

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2002, 08:26:16 ; Search time 13.41 Seconds

(without alignments)
1108.748 Million cell updates/sec

Title: US-09-853-918-30

Perfect score: 1935
Sequence: 1 MADYLSGGTGVPEDELTA.....MSAQIEGTVHGLSHYERKLY 384

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1858	95.0	514	1	IMD1_HUMAN
2	1839	94.1	514	1	IMD1_MOUSE
3	1655	84.7	514	1	IMD2_MESAU
4	1653	84.6	514	1	IMD2_HUMAN
5	1640	83.9	514	1	IMD2_MOUSE
6	1348.5	69.0	537	1	IMDH_DROME
7	1245.5	63.7	524	1	IMH3_YEAST
8	1238.5	63.4	523	1	IMH2_YEAST
9	1233.5	63.1	523	1	IMH1_YEAST
10	1206.5	61.7	521	1	IMH3_CANAL
11	1095.5	56.0	514	1	IMDH_LEIDO
12	1094.5	56.0	512	1	IMDH_TRYBB
13	1016	52.0	502	1	IMH2_ARATH
14	1007.5	51.5	503	1	IMH1_ARATH
15	1001	51.2	454	1	IMDH_PNECA
16	691.5	35.4	403	1	IMDH_AQUAE
17	649	33.2	490	1	IMDH_BACSU
18	627.5	32.1	513	1	IMDH_BACSU
19	624.5	31.9	488	1	IMDH_ACTICA
20	613.5	31.4	521	1	IMDH_CHLVI
21	610.5	31.2	529	1	IMDH_MYCTU
22	601	30.7	404	1	IMDH_BORBU
23	600.5	30.7	488	1	IMDH_ECOLI
24	600.5	30.7	529	1	IMDH_MYCLE
25	587.5	30.1	487	1	IMDH_PASMU
26	586.5	30.0	488	1	IMDH_HAETN
27	577	29.5	492	1	IMDH_STRPY
28	574	29.4	481	1	IMDH_HELPY
29	572	29.3	481	1	IMDH_HELPY
30	538	27.5	498	1	IMDH_RHTR
31	505	25.8	496	1	IMDH_METHA
32	491	25.1	485	1	IMDH_PYRAB
33	490.5	25.1	486	1	IMDH_PYRAB

34	490	25.1	485	1	IMDH_PYRAB
35	384.5	19.7	503	1	IMDH_TRIFO
36	348	17.8	479	1	Y143_MYCTU
37	344	17.6	345	1	GUAC_RAT
38	341	17.4	345	1	GUAC_HUMAN
39	331.5	17.0	356	1	GUAC_ASCSU
40	324	16.6	478	1	Y143_MYCLE
41	312	16.0	358	1	GUAC_CAEBL
42	306.5	15.7	346	1	GUAC_ECOLI
43	289.5	14.8	349	1	GUAC_BUCAL
44	188.5	9.6	375	1	Y110_MYCTU
45	168.5	8.6	375	1	Y110_MYCLE
46	118.5	6.1	238	1	HIS4_METVA
47	116.5	6.0	442	1	GLXD_RHME
48	115.5	5.9	311	1	PYRD_BACSU
49	114.5	5.9	313	1	PYRD_BACCL
50	109	5.6	1888	1	CALE_CHICK
51	106.5	5.4	163	1	Y22B_HAETN
52	106	5.4	360	1	ID12_HALNI
53	105.5	5.4	393	1	MDLB_PSEBU
54	105.5	5.4	572	1	DEYL_HUMAN
55	104	5.3	239	1	HIS4_METH
56	104	5.3	378	1	ZMPD_NEUCR
57	103.5	5.3	624	1	SERA_ARATH
58	103	5.3	393	1	LA2M_MYCSM
59	102.5	5.2	290	1	PYRD_SULSO
60	102	5.2	306	1	PYRD_METHA
61	102	5.2	353	1	HAO3_HUMAN
62	101.5	5.2	569	1	URE1_BACRA
63	100.5	5.1	572	1	DEYL_MOUSE
64	100.5	5.1	252	1	DEYL_RAT
65	99.5	5.1	572	1	HIS6_RHOCA
66	99	5.1	238	1	HIS4_METHL
67	99	5.1	349	1	ID12_BACCU
68	98.5	5.0	244	1	PIRE_BACCL
69	98.5	5.0	354	1	CHVE_AGRAR
70	98.5	5.0	373	1	MDHM_CHLRE
71	98	5.0	352	1	HAO3_RAT
72	97	5.0	311	1	MDH_VIRCH
73	97	5.0	367	1	GOX2_ARATH
74	96	4.9	267	1	HIS6_MYCTU
75	96	4.9	367	1	GOX1_ARATH
76	96	4.9	463	1	MORD_RHME
77	95	4.9	369	1	GOX_SPTOL
78	95	4.9	603	1	PURL_THEMA
79	94.5	4.8	253	1	PCRB_THEMA
80	94.5	4.8	449	1	ACCC_ECOLI
81	94.5	4.8	949	1	AHM6_ARATH
82	94.5	4.8	1556	1	GLTS_SYNF3
83	94	4.8	312	1	PYDB_ENTFA
84	94	4.8	351	1	HAO2_HUMAN
85	93.5	4.8	292	1	GTAB_BACSU
86	93.5	4.8	299	1	PYRD_ARCTU
87	93.5	4.8	1180	1	PYC2_YEAST
88	93	4.8	281	1	TRPA_CORBL
89	93	4.8	306	1	PYRD_AQUAE
90	93	4.8	384	1	YB23_MYCLE
91	93	4.8	426	1	THCD_RHOBR
92	93	4.8	609	1	Y4PA_RHISN
93	92.5	4.7	211	1	THIE_BACDH
94	92.5	4.7	342	1	ID12_RICCN
95	92.5	4.7	401	1	HUTI_CAUDR
96	92.5	4.7	416	1	ATTY_TRYOR
97	92.5	4.7	661	1	BAIH_EUSBP
98	92	4.7	261	1	THIG_MYCLE
99	92	4.7	264	1	THIG_XYLFA
100	91.5	4.7	444	1	Y808_CHLBN

ALIGNMENTS

RESULT 1

P42851 pyrococcus
P50097 titrichomo
O50591 mycobacteri
O92424 rattus norv
P36599 homo sapien
P27442 ascaris suu
O32912 mycobacteri
O16294 caenorhabdi
P15344 escherichia
P57300 buchnera ap
O50716 mycobacteri
O49721 mycobacteri
P05324 methanococ
O87392 rhizobium m
P25996 bacillus m
P46539 bacillus ca
P32018 gallus galli
O86223 haemophilus
O93he4 halobacteri
P20932 pseudomonas
O14194 homo sapien
O26931 methanobact
O01284 neurospora
O04130 arabidopsis
P21795 mycobacteri
O9ux04 sulfolobus
O58070 methanococ
O9nyq2 homo sapien
P41020 bacillus pa
P97427 mus musculu
O62950 rattus norv
O30724 rhodospirer
O50757 methanococ
P50740 bacillus su
P46535 bacillus ca
P54082 agrobacteri
O42686 chlamydomon
O07523 rattus norv
O9uk13 vibrio chol
O91rr9 arabidopsis
O53908 mycobacteri
O91r80 arabidopsis
O52953 rhizobium m
P05414 spinacia ol
O9ux03 thermotoga
O9hjh3 thermoplasma
P24182 escherichia
O9s2c9 arabidopsis
P55038 synechocyst
O47741 enterococcu
O9nyq3 homo sapien
O05852 b utp--gluc
O23513 archaeoglob
P33277 saccharomyc
P06562 synechocyst
O65461 aquifex aeo
O50049 mycobacteri
P43494 rhodococcus
P56610 rhizobium s
O9nyh7 bacillus ha
O92hm7 rickettsia
P58079 calobacter
P33447 trypanosoma
P32332 eubacterium
O92b12 mycobacteri
O96f95 xyella fas
O92798 chlamydia p

IMDL_HUMAN
 ID IMDL_HUMAN STANDARD: PRT; 514 AA.
 AC P20839;
 DT <01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inosine-5'-monophosphate dehydrogenase 1 (EC 1.1.1.205) (IMP
 dehydrogenase 1) (IMPDH-1) (IMPDH 1).
 GN IMPDH1 OR IMPD1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBL_TaxID=9606;
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RX MEDLINE=90203022; PubMed=1969416;
 RA Matsushima Y., Ohno S., Kawasaki H., Konno Y., Weber G., Suzuki K.;
 RT "Two distinct cDNAs for human IMP dehydrogenase.";
 RL J. Biol. Chem. 265:5292-5295(1990).
 RN
 RP CHARACTERIZATION.
 RA MEDLINE=95283610; PubMed=7763314;
 RX Hager P.W., Collart F.R., Huberman E., Mitchell B.S.;
 RT "Recombinant human inosine monophosphate dehydrogenase type I and
 RT type II proteins. Purification and characterization of inhibitor
 RT binding.";
 RL Biochem. Pharmacol. 49:1323-1329(1995).
 CC -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
 CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
 CC OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF
 CC MALIGNANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.
 CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
 CC xanthosine 5'-phosphate + NADH.
 CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- TISSUE SPECIFICITY: IMP TYPE I IS THE MAIN SPECIES IN NORMAL
 CC LEUCOCYTES AND TYPE II PREDOMINATES OVER TYPE I IN THE TUMOR.
 CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 CC GMP REDUCTASE.
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
 CC
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 CC
 CC EMBL; J05272; AAA36114.1; ALT_SEQ.
 DR PIR; A35566; A35566.
 DR HSSP; P12268; 1B30.
 DR MIM; 146690; -
 DR InterPro; IPR000644; CBS.
 DR InterPro; IPR003009; FMN_enzyme.
 DR InterPro; IPR001093; IMP_DH_GMP_RED.
 DR Pfam; PF00571; CBS_2.
 DR Pfam; PF00478; IMPDH_C_1.
 DR Pfam; PF01574; IMPDH_N_1.
 DR SMART; SM00116; CBS_2.
 DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
 KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
 KW Multigene family; Repeat; CBS domain.
 FT DOMAIN 112 CBS 1.
 FT DOMAIN 177 CBS 2.
 FT BINDING 331 IMP (POTENTIAL)
 SQ SEQUENCE 514 AA; 55449 MW; 751303f8e9e21061 CRC64;

QY 1 MADDYISGTYGYPEDEGLTAQQLFASADGLTYNDPILGFIIDEVDELTSALTRKIT 60
 DB 1 MADDYISGTYGYPEDEGLTAQQLFASADGLTYNDPILGFIIDEVDELTSALTRKIT 60
 QY 61 LKTPPLISSPMDTYTEADMAIAMLGMGIGFIHNHCTPEEQANVRKVKFD----- 111
 DB 61 LKTPPLISSPMDTYTEADMAIAMLGMGIGFIHNHCTPEEQANVRKVKKEGGFITDPVY 120
 QY 112 ----- 111
 DB 121 LSPSHVGVYLEAKMRHGSFGITETGTMGSKLVGIVTSRODIFLAEKDHITLSEVWT 180
 QY 112 ----- 111
 DB 181 PRIELVAPAGVTLKEANEILQSRKKGLPIYNDCELVAIIARTDLKKNRDYPLASKDS 240
 QY 112 -KTLGGAANGVREDKRYRLDLLTQAGVYIVYDSSQGSVYQIAVWHYTKQYPLQYI 170
 DB 241 QKOLLGGAANGVREDKRYRLDLLTQAGVYIVYDSSQGSVYQIAVWHYTKQYPLQYI 300
 QY 171 GGNVYTAQAQKNLIDAGVGLRVGMCGSICITQEVMACGRPGGTAVYVAEYARRFGVP 230
 DB 301 GGNVYTAQAQKNLIDAGVGLRVGMCGSICITQEVMACGRPGGTAVYVAEYARRFGVP 360
 QY 231 IADGSIQYGVHVKALALGASTVMKSLAATTEAPGEFFSDGYRLKKYRGMSLDM 290
 DB 361 IADGSIQYGVHVKALALGASTVMKSLAATTEAPGEFFSDGYRLKKYRGMSLDM 420
 QY 291 EKSSSOKRFESGDKVYKIAQGVSGSIQDKGSIQKQVPTLIAGIQCQDIGARSISVLR 350
 DB 421 EKSSSOKRFESGDKVYKIAQGVSGSIQDKGSIQKQVPTLIAGIQCQDIGARSISVLR 480
 QY 351 SMWYSGELKFEKRTMSAQIEGCVHGLSHYEKRLY 384
 DB 481 SMWYSGELKFEKRTMSAQIEGCVHGLSHYEKRLY 514

RESULT 2
 ID IMDL_MOUSE STANDARD: PRT; 514 AA.
 AC P50096;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Inosine-5'-monophosphate dehydrogenase 1 (EC 1.1.1.205) (IMP
 dehydrogenase 1) (IMPDH-1) (IMPDH 1).
 GN IMPDH1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBL_TaxID=10090;
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukemia;
 RA Dayton J.S., Mitchell B.S.;
 RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
 CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
 CC OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF
 CC MALIGNANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.
 CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
 CC xanthosine 5'-phosphate + NADH.
 CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 CC GMP REDUCTASE.
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
 CC
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DR EMBL: U00978; AAA18285.1; -
 DR HSSP: P12268; 1B30.
 DR MGD: MGI:96567; Impdh1.
 DR InterPro: IPR000644; CBS.
 DR InterPro: IPR003009; FMN_enzyme.
 DR InterPro: IPR001093; IMP_DH_GMP_RED.
 DR Pfam: PF00571; CBS; 2.
 DR Pfam: PF00478; IMPDH_C; 1.
 DR Pfam: PF01574; IMPDH_N; 1.
 DR SMART: SM00116; CBS; 2.
 DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
 DR Oxidoreductase: NAD: GMP biosynthesis; Purine biosynthesis;
 KM Multigene family; Repeat: CBS domain.
 FT DOMAIN 112 167 CBS 1.
 FT BINDING 177 232 CBS 2.
 FT BINDING 331 331 IMP (POTENTIAL).
 SQ SEQUENCE 514 AA; 55294 MW; B38AA2EB0EC64CE CRC64;

Query Match 94.1%; Score 1839; DB 1; Length 514;
 Best Local Similarity 72.8%; Pred. No. 3.9e-131;
 Matches 374; Conservative 6; Mismatches 4; Indels 130; Gaps 1;

QY 1 MADYLLSGTGYVPEDGLTAQOLFASADGLTYNDPILPGFIDFIDEVDLSALTKKIT 60
 DB 1 MADYLLSGTGYVPEDGLTAQOLFASADGLTYNDPILPGFIDFIDEVDLSALTKKIT 60
 QY 61 LKTPLLSSPMDVTEADMAIAMAIMGIGFIHNCNTPFOANEVRKVKED----- 111
 DB 61 LKTPLLSSPMDVTEADMAIAMAIMGIGFIHNCNTPFOANEVRKVKED----- 111
 QY 112 ----- 111
 DB 121 LSPSHVGVDLBAKIQHGFSGIPITATGTMSKLVGIVTSRDIDFLAEKDHITLSEVMT 180
 QY 112 ----- 111
 DB 181 PREVELVAPAGVTLKANEILORSKKGKPIYNDDELVAIIARTDLKKNRDYPLASKDS 240
 QY 112 -KTLGGAAGVTRREDDKYRLDLTQAGVDVIVLDSQGSNSVQIAMVHYIKOKYPHLYI 170
 DB 112 -KTLGGAAGVTRREDDKYRLDLTQAGVDVIVLDSQGSNSVQIAMVHYIKOKYPHLYI 170
 QY 241 HROLGGAAGVTRREDDKYRLDLTQAGVDVIVLDSQGSNSVQIAMVHYIKOKYPHLYI 300
 DB 241 HROLGGAAGVTRREDDKYRLDLTQAGVDVIVLDSQGSNSVQIAMVHYIKOKYPHLYI 300
 QY 171 GGNVYTAAGAKNLIDAGVGLKRVGCGSICITQEVMACGRPGTAVVYAEYARFEGVP 230
 DB 301 GGNVYTAAGAKNLIDAGVGLKRVGCGSICITQEVMACGRPGTAVVYAEYARFEGVP 230
 QY 231 IADGIGTGVHVKALAGASTVMMGSLAATTEAEGEYFPFSDGVRLLKRYGMSLDAM 290
 DB 361 VADGGIGTGVHVKALAGASTVMMGSLAATTEAEGEYFPFSDGVRLLKRYGMSLDAM 420
 QY 291 EKSSSSQKRYFSEGDVKYIAQVSGSIOQKSIQKFPYLLAGIQHCODIGARSLVLR 350
 DB 421 EKSSSSQKRYFSEGDVKYIAQVSGSIOQKSIQKFPYLLAGIQHCODIGARSLVLR 480
 QY 351 SMYSGELKFEKRTMSAQIEGCVHGLHSTYERKLY 384
 DB 481 SMYSGELKFEKRTMSAQIEGCVHGLHSTYERKLY 514
 RESULT 3
 ID2_MESAU STANDARD; PRT; 514 AA.
 AC P12269;
 DT 01-OCT-1989 (rel. 12, Created)
 DT 01-OCT-1989 (rel. 12, Last sequence update)
 DT 01-NOV-1997 (rel. 35, Last annotation update)
 DE Inosine 5'-monophosphate dehydrogenase 2 (EC 1.1.1.205) (IMP
 dehydrogenase 2) (IMPDH-II) (IMPD 2).

GN IMPDH2 OR IMPDH.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxId=10036;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 336-370.
 RX MEDLINE=89008491; PubMed=2902093;
 RA Collart F.R., Huderman E.;
 RT "Cloning and sequence analysis of the human and Chinese hamster
 RT Inosine-5'-monophosphate dehydrogenase cDNAs.";
 RL J. Biol. Chem. 263:15769-15772(1988).
 CC -!- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
 CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
 CC OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF
 CC MALIGNANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.
 CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NADH.
 CC -!- XANTHOSINE 5'-PHOSPHATE + NADH.
 CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
 CC -!- SUBUNIT: HOMOTETRAMER.
 CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 CC GMP REDUCTASE.
 CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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DR EMBL: J04209; AAA36993.1; -
 DR PIR: B31997; B31997.
 DR HSSP: P12268; 1B30.
 DR InterPro: IPR000644; CBS.
 DR InterPro: IPR003009; FMN_enzyme.
 DR InterPro: IPR001093; IMP_DH_GMP_RED.
 DR Pfam: PF00571; CBS; 2.
 DR Pfam: PF00478; IMPDH_C; 1.
 DR Pfam: PF01574; IMPDH_N; 1.
 DR SMART: SM00116; CBS; 2.
 DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
 DR Oxidoreductase: NAD: GMP biosynthesis; Purine biosynthesis;
 KM Multigene family; Repeat: CBS domain.
 FT DOMAIN 112 167 CBS 1.
 FT BINDING 177 232 CBS 2.
 FT BINDING 331 331 IMP (POTENTIAL).
 SQ SEQUENCE 514 AA; 55890 MW; 5FA0138FA41E8A02 CRC64;
 Query Match 84.7%; Score 1655; DB 1; Length 514;
 Best Local Similarity 63.6%; Pred. No. 2.7e-117;
 Matches 327; Conservative 31; Mismatches 26; Indels 130; Gaps 1;
 QY 1 MADYLLSGTGYVPEDGLTAQOLFASADGLTYNDPILPGFIDFIDEVDLSALTKKIT 60
 DB 1 MADYLLSGTGYVPEDGLTAQOLFASADGLTYNDPILPGFIDFIDEVDLSALTKKIT 60
 QY 61 LKTPLLSSPMDVTEADMAIAMAIMGIGFIHNCNTPFOANEVRKVKED----- 111
 DB 61 LKTPLLSSPMDVTEADMAIAMAIMGIGFIHNCNTPFOANEVRKVKED----- 111
 QY 112 ----- 111
 DB 121 LSPKRVDRVDFEAKAHGFCGIPITDTGRMGRVGLIISRDIIDFLKEEHDRIEIMT 180
 QY 112 ----- 111
 DB 181 KREDLVVAPAGITLKANEILORSKKGKPIYNDDELVAIIARTDLKKNRDYPLASKDA 240
 QY 112 -KTLGGAAGVTRREDDKYRLDLTQAGVDVIVLDSQGSNSVQIAMVHYIKOKYPHLYI 170

```

Db 241 KQOLLCGAAIGTHEDDXYRDLDLALAGVYVLDSSQGNSTFQJNMKIMKEKTPNLQVY
QY 171 GGNVYTAQAQKNLIDAGVDL RVMGCGSICITQEVACGRPOGTAVYKYAEVAREGVP 230
Db 301 GGNVYTAQAQKNLIDAGVDL RVMGCGSICITQEVACGRPOGTAVYKYAEVAREGVP 360
QY 231 IADGGIQTGYGHVYKALALASTVMGSLAATTEAPGEYFFSDGVRLKRYRGMSLDAM 290
Db 361 VADGGIQTGYGHVYKALALASTVMGSLAATTEAPGEYFFSDGVRLKRYRGMSLDAM 420
QY 291 EKSSSOKRFESEGDYKRIQGVSGSIQDKSGIOPVYPIAGIOHCODIGARSLSVLR 350
Db 421 DKHSSONRFTSEADKTKVQGVSGAVQDQSGIHKFVYPIAGIQHSCODIGAKSLTVOR 480
QY 351 SMWYSGELKEFKRTMSAOIEGVGVLHSYERKLY 384
Db 481 AMWYSGELKEFKRTSSAQVEGVHSLHSYERKLF 514

RESULT 4
IMD2_HUMAN
ID IMD2_HUMAN STANDARD; PRT; 514 AA.
AC P12268;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase 2 (EC 1.1.1.205) (IMP
DE dehydrogenase 2) (IMPDH-II) (IMPDH 2).
GN IMPDH2 OR IMPD2.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=89008491; PubMed=2902093;
RA Collart F.R., Huberman E.;
RT "Cloning and sequence analysis of the human and Chinese hamster
RT Inosine-5'-monophosphate dehydrogenase cDNAs.";
RL J. Biol. Chem. 263:15769-15772(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=90203022; PubMed=1969416;
RA Natsumeda Y., Ohno S., Kawasaki H., Konno Y., Weber G., Suzuki K.;
RT "Two distinct cDNAs for human IMP dehydrogenase.";
RL J. Biol. Chem. 265:5292-5295(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95091778; PubMed=7999076;
RA Giesne D.A., Huberman E.;
RT "Cloning and sequence of the human type II IMP dehydrogenase gene.";
RL Biochem. Biophys. Res. Commun. 205:537-544(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95204479; PubMed=7896827;
RA Zimmermann A.G., Sychala J., Mitchell B.S.;
RT "Characterization of the human Inosine-5'-monophosphate dehydrogenase
RT type II gene.";
RL J. Biol. Chem. 270:6808-6814(1995).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=95283610; PubMed=7763314;
RA Hager P.W., Collart F.R., Huberman E., Mitchell B.S.;
RT "Recombinant human Inosine monophosphate dehydrogenase type I and
RT type II proteins. Purification and characterization of inhibitor
RT binding.";
RL Biochem. Pharmacol. 49:1323-1329(1995).
RN [6]
RX X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE=99199217; PubMed=10097070;

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RA Colby T.D., Vanderveen K., Strickler M.D., Markham G.D.,
RA Goldstein B.M.;
RT "Crystal structure of human type II inosine monophosphate
RT dehydrogenase: implications for ligand binding and drug design.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:3531-3536(1999).
CC -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
CC OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF
CC MALIGNANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- TISSUE SPECIFICITY: IMP TYPE I IS THE MAIN SPECIES IN NORMAL
CC LEUKOCYTES AND TYPE II PREDOMINATES OVER TYPE I IN THE TUMOR.
CC -1- PTM: The N-terminus is blocked.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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DR EMBL: J04208; AAA36112.1; -
DR EMBL: L33842; AAA67054.1; -
DR EMBL: L39210; AAB70699.1; -
DR PIR: A31997; A31997.
DR PIR: B35566; B35566.
DR PDB: 1B30; 12-APR-99.
DR MIM: 146691; -
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
KW Multigene family; Repeat; CBS domain; 3D-structure.
FT DOMAIN 112 167 CBS 1.
FT DOMAIN 177 232 CBS 2.
FT BINDING 331 331 IMP (POTENTIAL).
FT CONFLICT 190 191 AC -> RS (in Ref. 1).
SQ SEQUENCE 514 AA; 55805 MW; 876BEA0EC1DDBE9 CRC64;

Query Match 84.6%; Score 1653; DB 1; Length 514;
Best local Similarity 63.8%; Pred. No. 3,9e-117;
Matches 328; Conservative 29; Mismatches 27; Indels 130; Gaps 1;

QY 1 MADYLLISGTVPEDEGLTAQQLFASADGLTYNDFLLPGEIDFIADVDLSALTRKIT 60
Db 1 MADYLLISGTVPEDEGLTAQQLFASADGLTYNDFLLPGEIDFIADVDLSALTRKIT 60
QY 61 LKTPILSSPMDTYTEADMAIAMLGMGIGFIHNCIPEPOANVRKVKPPD----- 111
Db 61 LKTPILSSPMDTYTEADMAIAMLGMGIGFIHNCIPEPOANVRKVKPPD----- 111
QY 112 ----- 111
Db 121 LSPKRDVRYDFEAKARHGCIGITDTGRMGSLVGISSRQIDFLKEEHDFLEIMT 180
QY 112 ----- 111
Db 181 KREDLVVAPAGITLKEANETLQSRKKGKLPYVNEDELVAIARTDLKKNRDPVPLASKDA 240
QY 112 -KTLGCAAVGTREDDKRYRLDLTLQAGVDVYIVLDSSQGNSTVQIADVHYIKQKYPHLQVY 170

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Db 241 KRÖLLCGAIGTHEDDKYRLDLAAGVVDVLDSSQNSISIPQIMKIKYKPNLQYI 300
Oy 171 GGNVYTAQAQAKLIDAGVDGLRVGMCSSICTOEVMACGRPGTAAYVVAETARFGVP 230
Db 301 GGNVYTAQAQAKLIDAGVDALRVGMSGSSICTOEVLACGRPOATVAVKVSERARFGVP 360
Oy 231 IADGCIQVGHVAVKALAGASTVMGSLAATTEAPGEFFSDGVRLLKRYGMSLDM 290
Db 361 VIADGCIQVGHVAVKALAGASTVMGSLAATTEAPGEFFSDGVRLLKRYGMSLDM 420
Oy 291 EKSSSSQKRYESEGDKVKIAGVSSGIDKSGIQKFPVPLIAGIHCODIGARSLVLR 350
Db 421 DKHLSSQNRFESEADKIKVAGVSGAVODKSGIHKFPVPLIAGIHCODIGAKSLTVGR 480
Oy 351 SMVSGELKFEKRTMSAQIEGSGVHLSYERKLY 384
Db 481 AMVSGELKFEKRTSSAQVEGSGVHLSYERKLY 514

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RESULT 5

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IMD2_MOUSE STANDARD: PRT: 514 AA.
ID IMD2_MOUSE STANDARD: PRT: 514 AA.
AC P24547: Q61734;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase 2 (EC 1.1.1.205) (IMP
DE dehydrogenase 2) (IMPDH-II) (IMPD 2).
GN IMPDH2 OR IMPDH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91153661; PubMed=1671845;
RA Tiedeman A.A., Smith J.M.;
RL "Isolation and sequence of a cDNA encoding mouse IMP dehydrogenase.";
RL Gene 97:289-293(1991).
RN [2]
RP SEQUENCE FROM N.A. AND VARIANTS MYCOPHENOLIC ACID RESISTANT.
RC TISSUE=Brain;
RX MEDLINE=94153991; PubMed=7906545;
RA Lightfoot T., Snyder F.F.;
RL "Gene amplification and dual point mutations of mouse IMP
RL dehydrogenase associated with cellular resistance to mycophenolic
RL acid."
RL Biochim. Biophys. Acta 1217:156-162(1994).
CC -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
CC OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF
CC MALIGNANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.
CC -1- CATALYTIC ACTIVITY: THE GROWTH PROGRESSION OF SOME TUMORS.
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
DR EMBL: M33934; AAA39311.1;
DR EMBL: M98333; AAA20181.1;
DR PIR: J70565; J70565.
DR HSP: P12268; I830.

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DR MGD: MGI:109367; Impdh2.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
KW Multigene family; Repeat; CBS domain.
FT DOMAIN 112 167 CBS 1.
FT DOMAIN 177 232 CBS 2.
FT BINDING 331 331 IMP (POTENTIAL).
FT VARIANT 333 333 T -> I (IN MYCOPHENOLIC ACID RESISTANT
FT CELLS).
FT VARIANT 351 351 S -> Y (IN MYCOPHENOLIC ACID RESISTANT
FT CELLS).
FT CONFLICT 483 483 T -> M (IN REF. 2).
SQ SEQUENCE 514 AA; 55785 MW; D5B6A5C5EBCC421 CRC64;

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Query Match 83.9%; Score 1640; DB 1; Length 514;
Best Local Similarity 63.4%; Pred. No. 3.7e-116;
Matches 326; Conservative 29; Mismatches 29; Indels 130; Gaps 1;

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Oy 1 MADYILISGGTGVPPDGLTAQDLFASADGLVYNDFLILPGFLDAEDVLSALTRKT 60
Db 1 MADYILISGGTGVPPDGLTAQDLFASADGLVYNDFLILPGFLDAEDVLSALTRKT 60
Oy 61 LKTPILISSMDPTVTEADNAIAMAALNGIGIGIHNCTPEFOANEVRKVKFD----- 111
Db 61 LKTPILISSMDPTVTEADNAIAMAALNGIGIGIHNCTPEFOANEVRKVKVKFD----- 111
Oy 61 LKTPILISSMDPTVTEADNAIAMAALNGIGIGIHNCTPEFOANEVRKVKVKFD----- 111
Db 61 LKTPILISSMDPTVTEADNAIAMAALNGIGIGIHNCTPEFOANEVRKVKVKFD----- 111
Oy 112 ----- 111
Db 121 LSPKDRVDFEAKARHFGCGIPITDTGRMSRLVGIISRDIDELKEEDHDFLEIMT 180
Oy 112 ----- 111
Db 181 KREDLVAPAGTYLKEANFIILORSKKKRLPIYNEDELVAIITARDLKKRNDYPLASKDA 240
Oy 112 -KTLGGAAGVTRDEDDKYRLDLTAQVDVYLDSSQNSVYQIAMVHYIKOKYRPHLOYI 170
Db 241 KRÖLLCGAIGTHEDDKYRLDLAAGVVDVLDSSQNSISIPQIMKIKYKPNLQYI 300
Oy 171 GGNVYTAQAQAKLIDAGVDGLRVGMCSSICTOEVMACGRPGTAAYVVAETARFGVP 230
Db 301 GGNVYTAQAQAKLIDAGVDALRVGMSGSSICTOEVLACGRPOATVAVKVSERARFGVP 360
Oy 231 IADGCIQVGHVAVKALAGASTVMGSLAATTEAPGEFFSDGVRLLKRYGMSLDM 290
Db 361 VIADGCIQVGHVAVKALAGASTVMGSLAATTEAPGEFFSDGVRLLKRYGMSLDM 420
Oy 291 EKSSSSQKRYESEGDKVKIAGVSSGIDKSGIQKFPVPLIAGIHCODIGARSLVLR 350
Db 421 DKHLSSQNRFESEADKIKVAGVSGAVODKSGIHKFPVPLIAGIHCODIGAKSLTVGR 480
Oy 351 SMVSGELKFEKRTMSAQIEGSGVHLSYERKLY 384
Db 481 AMVSGELKFEKRTSSAQVEGSGVHLSYERKLY 514

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RESULT 6

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IMDH_DROME STANDARD: PRT: 537 AA.
ID IMDH_DROME STANDARD: PRT: 537 AA.
AC Q07152: Q26455; Q9W2R8;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD) (Rasberry protein).
GN RAS OR CG1799.

```

OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nash D., Hu S.;
 RT "Drosophila inosine monophosphate dehydrogenase is encoded at the
 RT resperry locus."
 RL (in) Abstracts of the 35th meeting of the Canadian Federation of
 RL Biological Societies, pp.72-72, Victoria (1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94259281; PubMed=7911114;
 RA Nash D., Hu S., Leonard N.J., Tjong S.Y., Phillips D.;
 RT "The raspberry locus of Drosophila melanogaster includes an inosine
 RT monophosphate dehydrogenase like coding sequence."
 RL Genome 37:333-344(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CANTON-S;
 RX MEDLINE=94114565; PubMed=7904480;
 RA Sifri C.D., Wilson K., Smolik S., Forte M., Ullman B.;
 RT "Cloning and sequence analysis of a Drosophila melanogaster cDNA
 RT encoding IMP dehydrogenase."
 RL Biochim. Biophys. Acta 1217:103-106(1994).
 RN [4]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=96069715; PubMed=7476879;
 RA Stree R., Bownes M.;
 RT "The raspberry locus encodes Drosophila inosine monophosphate
 RT dehydrogenase."
 RL Mol. Gen. Genet. 248:755-766(1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sultion G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Adair J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegam C.,
 RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Murty D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazozo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
 CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
 CC OF CELL GROWTH.
 CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
 CC xanthosine 5'-phosphate + NADH.
 CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
 CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 CC GMP REDUCTASE.
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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 DR EMBL: L14847; AAA21831.1; -
 DR EMBL: L22608; AAA16839.1; -
 DR EMBL: S80430; AAB35628.1; -
 DR EMBL: AE003451; AAF46622.1; -
 DR HSSP: P12268; 1B30.
 DR FLYBase: Fgmd0003204; ras.
 DR InterPro: IPR000644; CBS.
 DR InterPro: IPR003009; FMN enzyme.
 DR InterPro: IPR001093; IMP_DH_GMP_RED.
 DR Pfam: PF00571; CBS; 2.
 DR Pfam: PF00478; IMPDH_C; 1.
 DR Pfam: PF01574; IMPDH_N; 1.
 DR SMART: SM00116; CBS; 2.
 DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
 KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
 KW CBS domain.
 KW CBS domain.
 FT DOMAIN 134 189
 FT 198 251
 FT BINDING 350 350
 FT BINDING 350 350
 FT CONFLICT 38 38
 FT CONFLICT 53 53
 FT CONFLICT 99 102
 FT CONFLICT 184 184
 FT CONFLICT 194 194
 FT CONFLICT 216 217
 FT CONFLICT 226 229
 FT CONFLICT 244 244
 FT CONFLICT 261 262
 FT CONFLICT 265 266
 FT CONFLICT 277 278
 FT CONFLICT 284 284
 FT CONFLICT 301 301
 FT CONFLICT 387 388
 FT SEQUENCE 537 AA; 57829 MW; A5EAB41AEAA64EBD CRC64;

Query Match 69.0%; Score 1348.5; DB 1; Length 537;
 Best local Similarity 53.5%; Pred. No. 3,3e-94;
 Matches 272; Conservative 53; Mismatches 50; Indels 133; Gaps 3;
 QY 10 TGTVPE-DGLTMOQLFASADGLTYDPLLPFGFIDFADVDLTLSALRKTKPLPLS 67
 DB 30 TCGDAELDIDLSCKELFQNEGLTYNDPLLPYIDFTEEDVLSPLTKSLTLRAPLVS 89
 QY 68 SPMDTVTEADMAIAMLGSGIFHNCPEPQANEVRYKRF----- 110
 DB 90 SPMDTVTESEMAIAMLALCGGIGIHHNCPEYQALEVHKYKKGKHPMDPSVMSPTNTY 149
 QY 111 ----- 110
 DB 150 GDVLEARRKNGFTGYPVTENGKLGKLLGWVTSRDIDPRENQEVLADIMTELTVAPR 209

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QY 111 -----DKTLGCAV 120
Db 210 GINLEPTANILEKSKKGLPIVNAQAGELVAMIAFTDLKARSYPNASKSNQLLVGA1 269
QY 121 GREDDEKRLDLTQAGVDVIVLDSOGNSVQIAMVHIKOKYIHLQVIGNVTAQA 180
Db 270 GRSDEKARLALLVANGVDIILDSOGNSVQVEMIKIKETPELOVIGNVTAQA 329
QY 181 KLIDAGVDGLRVGCGSICITQEVMAAGRPQGTAVYKVAAYARFPGPIIADGIOTV 240
Db 330 KLIDAGVDGLRVGCGSICITQEVMAAGCPQATAYVOSTYAKQFVPIADGIGT 389
QY 241 GHVYKALAGASTVMGSLAATTEAPGEFFPSDVRILKRYKRGMSLDAME----KSSSS 296
Db 390 GHVYKALAGASTVMGSLAATTEAPGEFFPSDVRILKRYKRGMSLDAMEGDAKGAAM 449
QY 297 OKRYSEGDVKVIAAGVSSIODKSGIOKFVYLLAGIOHGCODIGANSLSVRSMMSG 356
Db 450 SKRYHNEMDKMKVYAGVSSIVDKGSVLYRLPYLECGIOHSCODIGANSINLRDMYNG 509
QY 357 ELKFEKRTMSAOIEGCVHGLHSYERKLY 384
Db 510 QLRFKRTHSAQLEGVHGLHSYERKLF 537

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RESULT 7
ID IMH2_YEAST STANDARD: PRT: 524 AA.
AC P50094:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
dehydrogenase) (IMPDH).
GN YML056C OR YML935B.06C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Devlin K., Churcher C., Barrell B.G., Rajandream M.A.;
RL Submitted (NOV-1994) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
-1- xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIDR TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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-----
CC
DR EMBL: Z46729; CAAB6719.1; -
DR HSSP: P12268; I830.
DR SGD: S0004520; YML056C.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KM Hypothetical protein, Oxidoreductase, NAD; GMP biosynthesis;
KW Purine biosynthesis; Multigene family; Repeat; CBS domain.
FT DOMAIN 120 175 CBS 1.

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FT DOMAIN 183 235 CBS 2.
FT BINDING 336 336 IMP (POTENTIAL).
SQ SEQUENCE 524 AA; 56394 MW; A73D1E4EE8AED9 CRC64;

```

Query Match 63.7%; Score 1245.5; DB 1; Length 524;
 Best Local Similarity 49.0%; Pred. No. 1.8e-86;
 Matches 248; Conservative 58; Mismatches 67; Indels 133; Gaps 3;

```

QY 12 YPEEGRLAQAQAFASA--DGLTYNDPFLIPGIDPDAEDVLTSLTKITLTPLISSP 69
Db 18 YSSKDLVQLMDSTRTGGLTYNDPLPGLVNPPSSAVSLQTKTKITLTPFVSSP 77
QY 70 MDVTADMAIYALMALMGIGFTHNCTPEFQANEVRYKKKFD----- 111
Db 78 MDVTADMAIYALMALMGIGFTHNCTPEFQANEVRYKKKFD----- 111
QY 112 ----- 111
Db 138 VKMKRRKFGSGFPVTEDEKCPGLVGLVTSRDIQFLDEDSLIVSEVMTKNPVTKIGT 197
QY 112 -----KTLGCAVGT 122
Db 198 LKEGNEILKQTKKGLLIVDNGNLVSMLSRADLKNQNYPLASKSATTKQLLGAALGT 257
QY 123 REDDKYRLDLTQAGVDVIVLDSOGNSVQIAMVHIKOKYIHLQVIGNVTAQAQKN 182
Db 256 IEADKERLRLVEAGLDVIVLDSOGNSVQFQIAMVHIKOKYIHLQVIGNVTAQAQKN 317
QY 183 LIDAGVDGLRVGCGSICITQEVMAAGRPQGTAVYKVAAYARFPGPIIADGIGTGVH 242
Db 318 LIAAGADGLRIGMGSGSICITQEVMAAGRPQGTAVYKVAAYARFPGPIIADGIGTGVH 377
QY 243 VKKALAGASTVMGSLAATTEAPGEFFPSDVRILKRYKRGMSLDAMEKS----SSSK 298
Db 378 IYKALALGSSIVTMGSLAATTEAPGEFFPSDVRILKRYKRGMSLDAMEKSNKNAIS 437
QY 299 RFSEGDVKVIAAGVSSIODKSGIOKFVYLLAGIOHGCODIGANSLSVRSMMSG 358
Db 438 RFSESDSVLVAGVSGAVVNDKSGIKRFLPYLXNGIOHSCODIGESLTLKENVNGEV 497
QY 359 KEFKRTMSAOIEGCVHGLHSYERKLY 384
Db 498 REFRTASQALGCVHGLHSYERKLY 523

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RESULT 8
ID IMH2_YEAST STANDARD: PRT: 523 AA.
AC P50095:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
dehydrogenase) (IMPDH).
GN YLR432W OR L9753.4.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favello A., Fulton L., Gattung S., Greco T., Kirsten J.,
RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
RA Johnson D., Johnston L., Langston Y., Lettreille P., Le T.,
RA Mardis E., Menezes S., Miller N., Nhan N., Pauley A., Peluso D.,
RA Rifken L., Riles L., Tatch A., Trevisan E., Vignati D.,
RA Wilcox L., Wohlman P., Vaudin M., Watson R., Waterston R.,
RL Submitted (Feb-1995) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
-1- xanthosine 5'-phosphate + NADH.

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CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U01094; AAB67516.1; -.
DR HSSP: P12268; IB30.
DR SGD: S0004424; YLR432W.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
DR Hypothetical protein; Oxidoreductase; NAD; GMP biosynthesis;
KW Purine biosynthesis; Multigene family; Repeat; CBS domain.
FT DOMAIN 119 174 CBS 1.
FT BINDING 182 234 CBS 2.
FT BINDING 335 335 IMP (POTENTIAL).
SQ SEQUENCE 523 AA; 56584 MW; A0C84C2527AAEA6 CRC64;

Query Match 63.4%; Score 1238.5; DB 1; Length 523;
Best Local Similarity 48.6%; Pred. No. 6.1e-86;
Matches 244; Conservative 62; Mismatches 63; Indels 133; Gaps 3;

QY 16 DGLTAQOLFRS--ADGLTYNDFILPGEFDIADVDLTSALTRKTLKPLISSPMDTV 73
DB 21 DGLSVQELMSKIRGSLTYNDFILPGLVDFPSEVSLQTKLRNITLNLPIVSSPMDTV 80
QY 74 TEADMAIAMAIMGIGFIHNCPEFOANEVRKVKFD----- 111
DB 81 TESMAIFMALLGIGFIHNCPEQADAVRRKKNYENFINNPYISPTTYGEAKSM 140
QY 112 ----- 111
DB 141 KEREGSGFVTEDEKENGKLMGIVTSRDIOFVEDNSLIVQDWTKNPVGAOGITLSEG 200
QY 112 -----KTLGGAANGTRED 126
DB 201 NEILKTKKKKKLLIVDNGMLVMSLSTDLKMNQNPFLASKSATTKLGGALIGTIDAD 260
QY 127 KYRLDLTQAGVDVIVLDSQGSNVYQIAMVHYIKQKPYHLOYIGVNVVAAQAKNLIDA 186
DB 261 KERRLRLVEAGLDVILDSQGSNIFQLNMIKMKETFPDLEILAGVNAIRREQANLIAA 320
QY 187 GVGGLRVMGCGSICITQEVYACGPRQGTIVYVAEYARRPVPILADGSIQTVGHAVKA 246
DB 321 GAGGLRIGMGSGSICITQEVYACGPRQGTIVYVAYCEAFANFGIICMADGVQONIGHITKA 380
QY 247 LAIGASIVVMGSLLAATTEAPGEYFSDGVRLLKKYRGMGLDAMKES-----SSQKRYFS 302
DB 381 LAIGSIVVMGGMAGTETPGEYFODGRRLAAYRGMGIDAMQKTKGNASTRYFS 440
QY 303 EGDKVKIAQGVSGSIDQKSGIOKFPYLLAGIOHGCODICARSLSVLRSMYSGELFEK 362
DB 441 ESSSVLVAQGVSAVVDKSGIKKFIPLYLNGLOHSCODIGKSLTLKENVQSGKAVFER 500
QY 363 RTMSAQIEGGVHGLSHSEKRLY 384
DB 501 RTASAOLEGGVHNLHSEKRLH 522

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RESULT 9
ID IMH1_YEAST STANDARD; PRT; 523 AA.
AC P38697;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN PUR5 OR YHR216W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=528BC / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favello A., Fulton L., Gatlung S., Geisel C., Kirsten J.,
RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
RA Nhan M., Rifkin L., Riles L., St. Peter H., Trevasakis E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vaudin M.,
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VIII."
RL Science 265:2077-2082(1994).
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
DR EMBL: U00029; AAB6728.1; -.
DR PIR: S48997; S48997.
DR HSSP: P12268; IB30.
DR SGD: S0001259; PUR5.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
KW Multigene family; Repeat; CBS domain.
FT DOMAIN 119 174 CBS 1.
FT BINDING 182 234 CBS 2.
FT BINDING 335 335 IMP (POTENTIAL).
SQ SEQUENCE 523 AA; 7CA3BEC11238906B9 CRC64;

Query Match 63.1%; Score 1233.5; DB 1; Length 523;
Best Local Similarity 48.6%; Pred. No. 1.5e-85;
Matches 244; Conservative 62; Mismatches 63; Indels 133; Gaps 3;

QY 16 DGLTAQOLFRS--ADGLTYNDFILPGEFDIADVDLTSALTRKTLKPLISSPMDTV 73
DB 21 DGLSVQELMSKIRGSLTYNDFILPGLVDFPSEVSLQTKLRNITLNLPIVSSPMDTV 80
QY 74 TEADMAIAMAIMGIGFIHNCPEFOANEVRKVKFD----- 111

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RP SEQUENCE FROM N.A.
RA MEDLINE-9107664; PubMed-1671039;
RX Wilson K.E., Collart F.R., Huberman E., Stringer J.R., Ullman B.;
RT "Amplification and molecular cloning of the IMP dehydrogenase gene of
  Leishmania donovani."
RL J. Biol. Chem. 266:1665-1671(1991).
CC
CC -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
CC OF CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M55667; AAA29253.1; -
DR PIR: A38668; A38668.
DR HSSP: P12268; 1B30.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
DR Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KM CBS domain.
FT DOMAIN 110 165 CBS 1.
FT BINDING 172 228 CBS 2.
FT BINDING 327 377 IMP (POTENTIAL).
SQ SEQUENCE 514 AA; 55551 MW; E251FC1362D0E5 CRC64;

Query Match 56.0%; Score 1095.5; DB 1; Length 514;
Best Local Similarity 44.0%; Pred. No. 3.5e-75;
Matches 219; Conservative 62; Mismatches 88; Indels 129; Gaps 3;

QY 15 EDELTAQQLFASADGLTYNDFILPGRIDFIADENVDTLSLTRKITLTKPLISSPMQTVT 74
DB 14 KDCSTAEELF-KGDGLTYNDFILPGRIDFGADVNISGQFTKRIRLHIPVSSPMQTTT 72
QY 75 EADMAIATAMALMGIGFIHNCPEFOANEVRYKKF----- 110
DB 73 ENEMATMALMGVGVVLLHNCYERQVEMKSKATRNQISKPKSVPTPTISNIRK 132
QY 111 ----- 110
DB 133 EEKGISGIIIVTENGDPHGKLLGIYCTKIDIDYKKNKDPVSAMVTRREKMERAPQLLEE 192
QY 111 -----DKT--LLCGAANGREDD 126
DB 193 AMDVLRNRYGLPIVENEDEVNLCRRDAVARADYPHSTLDKSGRLCAATSTRPED 252
QY 127 KYRIIDLITQAGVDIVLDSQGSNVYQIAWHYIKOKYPHLOVYIGGVVYVTAQAOKNLIDA 186
DB 253 KRRVALADVDGVVLDVDSQGNITVQIATIKVVKSTPHLEVVAGNVVYQDQAKNLIDA 312
QY 187 GVDGLRVNGCGSICITQEVYMACRPGGTAVVYVAEYARREGVPIIADGCIQTVGHVYKA 246
DB 313 GADGIRIGMGSGSICITQEVYVACRPGGTAVVYVAEYARREGVPIIADGCIQTVGHVYKA 246
QY 247 LAIGASTVMMGSLAATTAAPGEGYFSDGVRLKTKYRGMSGLDMEKSSSSQKRYFSEGDK 306
DB 247 LAIGASTVMMGSLAATTAAPGEGYFSDGVRLKTKYRGMSGLDMEKSSSSQKRYFSEGDK 306

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DB 373 LAIGANCMALMGSLGTTPEFFEGYVRLKYRGMGSLDMEKSSQKRYFSEBENA 432
QY 307 VKIAGVSGSIDRKSIOKGFVPLVIGIOHCODIGARSISVLRSMYSGLFERRTMS 366
DB 433 VQVAGVSGNVVDRKSIAKIAVYVSKGLQDSADIGISPDALREKNYAGVLFRRSP 492
QY 367 AOTEGVGHLSYERKLY 384
DB 493 AOGEGVGHLSYERKLY 510

RESULT 12
ID IMPDH_TRYB STANDARD; PRT; 512 AA.
AC P50098;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
OS Trypanosoma brucei brucei.
OC Eukaryota; Euzoaria; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-EATRO 164 / ISTAT 1.7;
RX MEDLINE-95050714; PubMed-7961861;
RA Wilson K., Berens R.L., Sifri C.D., Ullman B.;
RT "Amplification of the inosinate dehydrogenase gene in Trypanosoma
RT brucei gambiense due to an increase in chromosome copy number."
RL J. Biol. Chem. 269:28979-28987(1994).
CC
CC -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
CC OF CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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CC -----
DR EMBL: M97794; AAB46420.1; -
DR HSSP: P12268; 1B30.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
DR Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KM CBS domain.
FT DOMAIN 108 163 CBS 1.
FT BINDING 170 226 CBS 2.
FT BINDING 325 375 IMP (POTENTIAL).
SQ SEQUENCE 512 AA; 55708 MW; 1A86C46AE445045 CRC64;

Query Match 56.0%; Score 1094.5; DB 1; Length 512;
Best Local Similarity 44.1%; Pred. No. 4.1e-75;
Matches 219; Conservative 66; Mismatches 83; Indels 129; Gaps 3;

QY 16 DGLTAQQLFASADGLTYNDFILPGRIDFIADENVDTLSLTRKITLTKPLISSPMQTVT 75
DB 16 DGLTAQQLFASADGLTYNDFILPGRIDFIADENVDTLSLTRKITLTKPLISSPMQTVT 75

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Db 13 DGTAAEEF-SQDGLSFNDPFIILPGFIDFSSKVNVSQFTKILLHLPLVSSPMDVTYE 71
Oy 76 ADMATAMLMGIGIFIHNCPEFOANFVRKYKF----- 110
Db 72 SSMAKAMLMGIGIVHNCPEFOANFVRKYKFIMKPKSVDPVSTIRNIKS 131
Oy 111 ----- 110
Db 132 EKGISGLVTEBGGKYDKGLLIVCTKIDFVKDASAPVSYMTRENTVERPIKLEEA 191
Oy 111 -----DKT-----LIGAAVGTREDDK 127
Db 192 MDVLRNRHGYLPVLDNDDEVVCLCSRDAVARADYPNSSLDNRHGLLCAATSTREADK 251
Oy 128 YRLDILTAGVAVYVLDSSQSNVYQIAMVHIKQYPHLOYIGNVVTAQAOKLIDAG 187
Db 252 GRVAALSRAGIDVLDSSQSNVYQIAMVHIKQYPHLOYIGNVVTAQAOKLIDAG 311
Oy 188 VDLGVNMGCGSICITQEVMAACGRPOGTAVYKVAEYARFVPIIADGIGTGVHVRAL 247
Db 312 ADSLRIGMGSSICITQEVMAACGRPOGTAVYKVAEYARFVPIIADGIGTGVHVRAL 371
Oy 248 ALGASTVMGSLAATTAPEGFYFSDVRLKTRMGSLDAMEKSSSSOKRYESEGKV 307
Db 372 AVGANVAMLGSMIACTSETPEYFEDKMDRLKGYRGMGSIDAMLOGRESGKYLESEETL 431
Oy 308 KIAQVSGSIDDKGSIQKQFVPLINGIOHGGODIGARSISVLRSMWYSGELKFEKRTMSA 367
Db 432 QVAGQVAGAVLDKGSVLLKLIHKGLOOSADIGEVSPDIREKVERGOVLFNRRTLTA 491
Oy 368 QIEGGVHGLHSEYKRLY 384
Db 492 QSEGAVHSLHMYERKLF 508

RESULT 13
IMH2_ARATH STANDARD: PRT: 502 AA.
AC 09SA34:
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
dehydrogenase) (IMPDH) (IMPDH).
GN AT1G16350 OR F309.15.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA.
RX MEDLINE=21016719; PubMed=11130712;
RA White O., Alonso J., Altarfi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Elgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gili J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huitzar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani A.,
RA Miltschker J., Miranda M., Nguyen M., Nierman M.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley B.I.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shin P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana."
RL Nature 408:816-820(2000).

```

```

CC -1 CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H2O =
CC xanthosine 5'-phosphate + NADH.
CC -1 PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1 SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1 SIMILARITY: CONTAINS 1 CBS DOMAIN.
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DR EMBL: AC006341; AAC34687.1; -.
DR HSSP: P12268; 1B30.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS. 1.
DR Pfam: PF00478; IMPDH_C. 1.
DR Pfam: PF01574; IMPDH_N. 1.
DR PROSITE: PS00487; IMP_DH_GMP_RED. 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain.
FT DOMAIN 167 219 CBS.
FT BINDING 321 321 IMP (POTENTIAL).
SO SEQUENCE 502 AA; 54051 MW; F887DB4160818310 CRC64;

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Query Match 52.0%; Score 1016; DB 1; Length 502;
Best local similarity 42.0%; Pred. No. 3,2e-69;
Matches 210; Conservative 61; Mismatches 97; Indels 132; Gaps 2;

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Oy 15 EDGLTAQQLFASADGLTYNDFILPGFIDFIDAEVDLTSAITRLTKTLTPLISSPMDVT 74
Db 5 EDGFSAEKLFSGQSYTYVDVFLPHFIDFSTDAVSLSTRKRVPLSLPCVASPMDTVS 64
Oy 75 EADMAIAMAALMGIGIFIHNCPEFOANFVRKYKF----- 110
Db 65 ESHMAAAMAALGIGIVHNCPEFOANFVRKYKFIMKPKSVDPVSTIRNIKS 124
Oy 111 ----- 110
Db 125 PSSFVFSQGTGLTPKRLGLGYSKSEMSMKDQKEVKIYDYKSCENKDYIYPMIDIDK 184
Oy 111 -----DKTLLCGAAVGTRE 124
Db 185 IEAVLEDKQKGFVLEKEGETVNVVTKDVERVKGYPKLSQTVGADKKMMVGAALGTRE 244
Oy 125 DDKYRLDILTAGVAVYVLDSSQSNVYQIAMVHIKQYPHLOYIGNVVTAQAOKL 184
Db 245 SKERLEHLYKAGANVAVVLDSSQSNVYQIAMVHIKQYPHLOYIGNVVTAQAOKL 304
Oy 185 DAGVGLLRVMGCGSICITQEVMAACGRPOGTAVYKVAEYARFVPIIADGIGTGVH 244
Db 305 KAGVGLLRVMGCGSICITQEVMAACGRPOGTAVYKVAEYARFVPIIADGIGTGVH 364
Oy 245 KALAGASTVMGSLAATTAPEGFYFSDVRLKTRMGSLDAMEKSSSSOKRYESEG 304
Db 365 KALVAGASTVMGSLAATTAPEGFYFSDVRLKTRMGSLDAMEKSSSSOKRYESEG 422
Oy 305 DKVTAQVSGSIDDKGSIQKQFVPLINGIOHGGODIGARSISVLRSMWYSGELKFE 364
Db 423 AKLKAQVAGVAVADKGSILKFIPTMAHVAKQGFIDGLASSLOSAAHLLRDMTLEART 482
Oy 365 MSAQIEGGVHGLHSEYKRLY 384
Db 483 GNAQIEGGVHGLHSEYKRSF 502

RESULT 14

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IMH1_ARATH STANDARD; PRT; 503 AA.
 AC P47996;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
 dehydrogenase) (IMPDH) (IMPD).
 GN IMPDH OR AT1G9470 OR T8K14.11.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=97045815; PubMed=8890737;
 RA Collart F.R., Ostlund J., Trent J., Olsen G.J., Huberman E.,
 RT "Cloning and characterization of the gene encoding IMP dehydrogenase
 from Arabidopsis thaliana."
 RL Gene 174:217-220(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Cressy T.H., Dewar K.,
 RA Dunn P., Egan P., Feldlyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hulzar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lanz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Malet R., Marshall A.,
 RA Miltner J., Miranda M., Nguyen M., Niemman W.C., Osborne B.I.,
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Souhwaick A.M.,
 RA Sun H., Taiton L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana."
 RL Nature 408:816-820(2000).
 CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
 CC xanthosine 5'-phosphate + NADH.
 CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
 CC -1- SIMILARITY: NO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 CC GMP REDUCTASE.
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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 DR EMBL: L34684; AAB41940.1; -
 DR EMBL: AC007202; AAD30229.1; -
 DR HSSP: P12268; I830.
 DR InterPro: IPR000644; CBS.
 DR InterPro: IPR003009; FMN_enzyme.
 DR InterPro: IPR001093; IMP_DH_GMP_RED.
 DR Pfam: PF00571; CBS_1.
 DR Pfam: PF00478; IMPDH_C_1.
 DR Pfam: PF01574; IMPDH_N_1.
 DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
 KW oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
 KW CBS domain.
 FT BINDING 322 322 IMP (POTENTIAL).

SQ SEQUENCE 503 AA; 54194 MW; ADDDAF9C3A697A9A CRC64;
 Query Match 51.5%; Score 1007.5; DB 1; Length 503;
 Best Local Similarity 42.1%; Pred. No. 1.4e-68;
 Matches 211; Conservative 62; Mismatches 95; Indels 133; Gaps 4;
 QY 15 EDGLTRAOQLFASADGLTYNDLILPGFIDFADEVDTLSATFRKTLKPLISSPMDTYT 74
 DB 5 EDGFPADKLFAQGYXYTDVIFLPFIIDSTFVAVSLSTRSRVPLISPCVSPMDTVS 64
 QY 75 EADMAIAMLMGSTGTHNC-----TFEFO----- 100
 DB 65 ESHMAAAMASLGGIGIVHNCIGIAQAASIIROAKSLKHPIASDAGVFPFEYETSLDAFG 124
 QY 101 ----- 100
 DB 125 PSSFVVEQTGYTTTKLLGYTKSQMKRMNTEQREMKIYDYMKSSDYCYPEIDE 184
 QY 101 -----ANEVRKKKFDK-----LLGAAVGR 123
 DB 185 KLEFVLEDKQKGFVLERDETVNVTYKDDIQVKGYPKSGGTGVPDGEEMVGAALGR 244
 QY 124 EDDKTYLDTLTOAGVDVYVLDSSQNSVYQIAMVHYKQYPLLOYTGNNVTAQAQKL 183
 DB 245 ESDKERLEHLVNVGVAVVLDSSQNSIYOLEIKIKVKKTYELDIGNVVTVQAQKL 304
 QY 184 IDAGVGLRVMGSGSICITQYFACRGROGTAIVYAVYARFPGVPIADGIGTGVH 243
 DB 305 IQAGVGLRVMGSGSICITQYFACRGROGTAIVYAVYARFPGVPIADGIGTGVH 364
 QY 244 VKALAGASTVMVMSLLAATTEAPGEYFSDGVRLLKRYMGSLDAEKSSSOKRFSF 303
 DB 365 VKALVGLASTVMVMSLLAATTEAPGEYFSDGVRLLKRYMGSLDAEKSSSOKRFSF 422
 QY 304 GDRVKTACGVSSGIDQKSGIOKFPVPLIAGIOHGCODIARSLSVLRSMYSGELAFER 363
 DB 423 QTRKLTAQGVAGVAAKGSVLILPYTHAVKGFQDLASSLSQSAHGLRSLNLRLEAR 482
 QY 364 TMSAQTEGVGHLSYERLY 384
 DB 483 TGAQVDEGVGHLSYERKSF 503
 RESULT 15
 ID IMDH_PNECA STANDARD; PRT; 454 AA.
 AC 012658;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
 dehydrogenase) (IMPDH) (IMPD).
 DE GNAI.
 OS Pneumocystis carinii.
 OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
 OC Pneumocystis.
 ON NCBI_Taxid=4754;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97135213; PubMed=8980752;
 RA O'Gara M.J., Lee C.H., Weinberg G.A., Nott J.M., Queener S.F.,
 RT "IMP dehydrogenase from Pneumocystis carinii as a potential drug
 target."
 RL Antimicrob. Agents Chemother. 41:40-48(1997).
 CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
 CC xanthosine 5'-phosphate + NADH.
 CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
 CC -1- SIMILARITY: NO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 CC GMP REDUCTASE.
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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Saccharomyces cerevisiae (baker's yeast).

[illegible]

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RESULT 17
ID IMDH_AOUAE STANDARD: PRT: 490 AA.
AC 067820;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMP).
GN CUAB OR AQ_2023.
OS Aquifex aeolicus.
OC Bacteria: Aquificales: Aquificaceae: Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5:
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Anjaj M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus".
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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CC -----
DR EMBL: AE000768; AAC07779.1; -.
DR HSSP: P50099; 1ZFY.
DR InterPro: IPR009644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS_2.
DR Pfam: PF00478; IMPDH_C_1.
DR Pfam: PF01574; IMPDH_N_1.
DR SMART: SM00116; CBS_2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KW oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain; Complete proteome.
FT DOMAIN 93 146 CBS 1.
FT DOMAIN 156 210 CBS 2.
FT BINDING 309 309 IMP (POTENTIAL).
SQ SEQUENCE 490 AA; 53400 MW; 66605CDBB8348CE4 CRC64;

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Query Match 33.2%; Score 649; DB 1; Length 490;
Best Local Similarity 33.2%; Pred. No. 1.3e-41;
Matches 157; Conservative 62; Mismatches 122; Indels 132; Gaps 3;

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QY 28 DGLTYNDLILPGFIDFIADVDLTSALRKRLTKPLISSPMDVTEDMAMALMG 87
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 10 EGLTFDVLIVPYSEVLPHVEDVSYTLKRIKLINIPYSAADVTETARLAIAREGG 69
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 88 IGTIHNCPEPGANVRYKKKFKDKLL----- 115
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 70 IGTIHNLPIKQAEVEYKKSEGMIIINPVTKPDTRYKALDIMAKYKISGVVDE 129
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 116 ----- 115
DB 130 EKKLIGLTNRDLRFTKPEDYSKPVSEPMTKENLITAPESITLDEADELFRKIKKLP 189
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

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QY 116 -----CGAAYGTREDDXRYRLDLLTQAGVDY 141
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 190 VDEKGIKGLITIKDLYKRRKKYPNACKDELGRLRVGAAGVTGETLDRVAALVEAGVDY 249
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 142 VLDSSOGNSVYQIAMHYTKOKTPHLQVIGGNVYTAQAKNLIDAGVDGLRGMCGGSGIC 201
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 250 VYDTAGHSKRRLVETETKIKANPEVDYIAGNAVTEGKRLALEADADAVKVGVPGSIC 309
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 202 IPEVWACGRPOGTAVYKVAEYARRPGVPIADGGIQTGVHVKALALASTVMMSILA 261
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 310 TTRIVAGVGPOLTAIMEANSAAREYDIPITADGIRYSGDIYKALAAAGSAVMGNLLA 369
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 262 ATTAPAGEYFFSDVRLKRYRCGSLDAMEKSSSKRYFESGDYKIAQVSGSIQDKG 321
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 370 GTEAPGETIYVYGRAYKRYRCGSLGAMSSRLSD-RYGOEKMEKFEVPEGIEGRVYRG 428
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 322 STOKFPYLIAGIHCODIGARSLVLSMYSGLKFEKFRMSQIIGVH 374
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 429 KLADVYVQLVGLRSGMGYVGARNIKELD-----KAKFVRLTWAGYRESHVH 476
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
RESULT 18
ID IMDH_BACSU STANDARD: PRT: 513 AA.
AC P21879;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMP) (Superoxide-inducible protein 12)
DE (S0112).
GN GUAB OR GNAB.
OS Bacillus subtilis.
OC Bacteria: Firmicutes: Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91067483; PubMed=1979163;
RA Kanazaki N., Miyagawa K.I.;
RT "Nucleotide sequence of the Bacillus subtilis IMP dehydrogenase
RT gene".
RL Nucleic Acids Res. 18:6710-6710(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96051385; PubMed=7584024;
RA Ogasawara N., Nakai S., Yoshikawa H.;
RT "Systematic sequencing of the 180 kilobase region of the Bacillus
RT subtilis chromosome containing the replication origin.";
RL DNA Res. 1:1-14(1994).
RN [3]
RP SEQUENCE OF 1-25.
RC STRAIN=ISS8;
RX MEDLINE=97443988; PubMed=9298659;
RA Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
RA Hecker M.;
RT "First steps from a two-dimensional protein index towards a response-
RT regulation map for Bacillus subtilis.";
RL Electrophoresis 18:1451-1463(1997).
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- INDUCTION: BY SUPEROXIDE.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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DR	EMBL: X55669; CAA39204.1; -
DR	EMBL: D26185; BAA05245.1; -
DR	EMBL: Z99104; CAB1785.1; -
DR	PIR: S12623; DEBSMP.
DR	HSSP: P50099; 1EFJ.
DR	Subtilist; BG10073; quab.
DR	InterPro: IPR000644; CBS.
DR	InterPro: IPR003009; FMN enzyme.
DR	InterPro: IPR001093; IMP_DH_GMP_RED.
DR	Pfam; PF00571; CBS; 2.
DR	Pfam; PF00478; IMPDH_C; 1.
DR	Pfam; PF01574; IMPDH_N; 1.
DR	SMART: SM00116; CBS; 2.
DR	PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KW	Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW	CBS domain; Complete proteome.
FT	DOMAIN 92 147 CBS 1.
FT	DOMAIN 155 209 CBS 2.
FT	BINDING 308 308 IMP (POTENTIAL).
FT	CONFLICT 28 28 H -> R (IN REF. 2).
FT	CONFLICT 480 513 VHRNKALDGLFSGHOKTGFVYDECCSGFFSSD ->
FT	KESENYNTS (IN REF. 2).
SEQ	SEQUENCE 513 AA; 55725 MW; 35D318E6DC51C89E CAC64;

```

DE Inosine 5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN GUBA.
OS Acinetobacter calcoaceticus.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
OX NCBI_TaxID=471;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EB 104;
RA Anderreg U., Schnuck W.H., Asperger O., Kleber H.-P.;
RL Submitted (JUN-1992) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIOUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
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[illegible][illegible]


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CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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CC -----
DR EMBL: 277165; CAB01012.1; -.
DR EMBL: AE007157; AAK47857.1; -.
DR HSSP: P12268; 1B30.
DR TIGR: M3519; -.
DR TruncatList: RV3411c; -.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
DR Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain; Complete proteome.
FT BINDING 341 341 IMP (POTENTIAL).
SQ SEQUENCE 529 AA; 54867 MW; 689A/C7C53993C0A CRC64;

Query Match 31.2%; Score 610.5; DB 1; Length 529;
Best Local Similarity 32.0%; Pred. No. 1;le-38;
Matches 158; Conservative 64; Mismatches 127; Indels 145; Gaps 10;

QY 2 ADVLISGCTGYPEDGLTAQQLFASAD-----GLTYNDFLLPGFIDEIADVDLTS 53
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 12 SDLVYS--PYRMGGLTTPDPTGDDPHKVMAMGLTFDDVLLPAASDVPAVPAATDTS 68
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 54 ALTKRITLKTPLISSPMDTYEADMATAMALMGIGFIHNN----- 94
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 69 QLTAKRIKLKPLVSSAMDTVESRMAIAMARAGMGVLRHRLPYAEQAGVEMVKRSEAG 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 95 -----CTPE----- 98
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 129 MYTPDPVTCRPNTLAQDALCARERISGLPYVDDGALVGLITNRDMFEVDQSKVAEV 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 99 -----FOANEVKK-----VKPKDKT----- 113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 189 MTKAPLITAGCGVSASALGLLRNRIKLELPVVDGRGLTGLTYKDPVKTEQHPPLATKD 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 114 -----LLCGAVGTREDDKYRLDLTQAGVDYIVLSSGNSVYQIAMVHYIKQY-PhLQ 168
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 249 SDRLGLVGAAGVGDANVRMMMLVDAGVDLVDTAHRRLVLDVWGKLKSEVGRVE 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 169 VIGNNVYTAQAOKLIDAGVDGLRYMGCGSICITQEVNACGPGQTVVYVAEYARBF 228
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 309 VVGAGNVATRSAAALVADAGAAVKGVGPGSICITRVVAGAGAQITAILLAVAACRAG 368
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 229 VPITADGGIQTGVHVAVALGASTVMGSLIAATTEAPGEYFSDGVRLLKRYMGSLD 288
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 369 VPVIADGGIQTGVHVAVALGASTVMGSLIAATTEAPGEYFSDGVRLLKRYMGSLD 428
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 289 AME-----KSSSSOKRPFSE-----DKYKIAAGVSSSIDKSIQKFFVYLLAGIOHGCOD 340
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 429 AMRGRGATYSKRDYFEDDALSEDKL-VPEGIEGRVFRKGPLSSVTHQLTGGLAAMGY 487
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 341 IGARSLVLRSMY 354
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 488 TGSPTIEVLQAQAF 501
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RESULT 22

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```

IMDH_BORBU
ID IMDH_BORBU STANDARD; PRT; 404 AA.
AC P49058;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine 5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN GNAB OR BBH17.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid cp26 (circular 26 kb).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; Pubmed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Iadigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochete, Borrelia
RT burgdorferi."
RL Nature 390:580-586(1997).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE=20222989; Pubmed=10758003;
RA McMillan F.M., Cahoon M., White A., Hedstrom L., Petsko G.A.,
RA Ringe D.;
RT "Crystal structure at 2.4-A resolution of Borrelia burgdorferi inosine
RT 5'-monophosphate dehydrogenase: evidence of a substrate-induced
RT hinged-lid motion by loop 6."
RL Biochemistry 39:4533-4542(2000).
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -----
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CC -----
DR EMBL: U13372; AAA53247.1; -.
DR EMBL: AE000792; AAC66314.1; -.
DR PDB: 1EEP; 29-MAR-00.
DR TIGR: BBH17; -.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Plasmid;
KW 3D-structure; Complete proteome.
FT BINDING 229 229 IMP.
SQ SEQUENCE 404 AA; 43767 MW; A91D6D6C5CE522P1 CRC64;

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Db      12 SDFVAS---SYRRLGGIMDDPAATGGGNPKRVAMLGTFEDVDVLLLPASDVNPATADISS 68
QY      54 ALFRKTLKPLTSPMDVTEADMAIAMLGIGIFHNH----- 94
Db      69 QLFKRIKRLKPLVSSAMDYTEARMALAMARAGMGVLRHNLFPVGCAGOVETVKSEAG 128
QY      95 -----CPE----- 98
Db      129 IMVTPYTCRPDNTLAQVGLCARFRISGLFVVDSDGALAGIITNRDMRFVDSKQVAV 188
QY      99 -----FOANEVRY-----VKKFDT----- 113
Db      189 MKRTPLTAAEGVSADALGLLRNRKIEKLPVVDGGRGLTGLTVXDEVTECHPLATKD 248
QY      114 -----LLCGAAGTREDDKYRLDLTQAGVVDVYLDSSQGSVYQIAMVHIKRY-PHLD 168
Db      249 NGRLLVGAAGVGGAWRAMMLVDAGVDVLTVDTAHNRLLVLDVKGKLEIGDRVQ 308
QY      169 VIGGNVNTAAQAKNLIDAGVDGLRVGSGSICITQEVMAAGRPCTAVYKVAEYARRFQ 228
Db      309 VIGGNVNTSAAALVAGADAVKGVGSGSTCTTRVAVGAPQITALEAVAACGPAG 368
QY      229 VPPIAAGGIGTGVHVKALALGASTVMGSLAATTEAPGEYFSSGVRLLKTRGMSLD 288
Db      369 VPIADGGIGLOYSIDIAKALAAAGSTMLGSLAGTAEAPELIFVNGKOFKSYRGMSLIG 428
QY      289 AME-----KSSSQKRYFSEK-----DKYIKAGVSGSIQKQKFPVYLIAGIQGCD 340
Db      429 AMGRGDKSYSKDRYFADALSEDKL-VPEGIEGRVPRFGLSVIHLVGLLRAMGY 487
QY      341 IGARSLSVLRSMY 354
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RESULT 25
IMDH_PASMO STANDARD; PRT; 487 AA.
AC 09L6B7;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
GN GUAB OR PM0295.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OX NCBI_TaxId=747;
RN [1]
RP SEQUENCE FROM N.A.
RA Fuller T.E., Kennedy M.J., Lowery D.E.;
RT "Identification of Pasteurella multocida virulence genes in a
RL septicemic mouse model using signature-tagged mutagenesis.";
RN Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=PM70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.U., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHER EOKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF237921; AAF68407.1; -.
CC DR EMBL; AE006064; AAK02379.1; -.
CC DR InterPro: IPR000644; CBS.
CC DR InterPro: IPR003009; FMN_enzyme.
CC DR InterPro: IPR001093; IMP_DH_GMP_RED.
CC DR Pfam; PF00571; CBS; 2.
CC DR Pfam; PF00478; IMPDH_C; 1.
CC DR Pfam; PF01574; IMPDH_N; 1.
CC DR SMART; SM00116; CBS; 2.
CC DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
CC Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
CC CBS domain; Complete proteome.
CC KW DOMAIN 91 144 CBS 1.
CC FT DOMAIN 153 206 CBS 2.
CC FT BINDING 305 305 IMP (POTENTIAL).
CC SO SEQUENCE 487 AA; 52007 MW; 0871DB0893B8FCA CRC64;

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Query Match 30.1%; Score 587.5; DB 1; Length 487;
Best local similarity 32.5%; Pred. No. 5,5e-37;
Matches 147; Conservative 59; Mismatches 114; Indels 133; Gaps 7;

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QY 28 DGLTVNDPILNGFIDFINDVDLTSLRKTITKPLTSPMDVTEADMAIAMLG 87
Db 7 EALTEDVDLVLPNASTVLTPLNADLSTQLTTRTNLPMLSAADVTEKRLSILOEG 66
QY 88 IGFHNCTPEFOANEVRKKFD----- 111
Db 67 IGFHNKMSIERQAEVRKVKKESGIVSDPYVSPTLSLAESELYKKNFASPPVVD 126
QY 112 -----KT----- 113
Db 127 EKNLVGITGRDTRFVTDLNKTVADEMPFKARLVTVKRNASDEIFGLMHTHREKVLV 186
QY 114 -----LLCGAAGTREDDKYRLDLTQAGVDVTV 142
Db 187 SDDFKLKGITTLKDVOKSEOKPOACKDERGLRVGAAGVAGCENERRIDALYKAGVDVLL 246
QY 143 LDSSQGSVYQIAMVHIKRYPHLOVIGNNVTTAAQAKNLIDAGVDGLRVGSGSICI 202
Db 247 IDSSHSGSVLQVRVETRAKYPDLPIVAGNVATAGALALADAGSAVKVIGPGSICT 306
QY 203 TOEVMACGRPGCTAVYKVAEYARRGVPIIADGGIGTGVHVKALALGASTVMGSLAA 262
Db 307 TRIVTGVGPQITAIADAAEALKDRGIPVIADGGIRFSGDISKALAAAGSCVMVSMFAG 366
QY 263 TTEAPGEYFPFSGVRLKRVKRGMSLDAMEKSSSQKRYF---SEGDKVIAAGVSSIDD 319
Db 367 TEAPGEIELYGRAFKSRGMSLGAMKSSSD--RIFQSDMAADKL-VPEIGIRIPY 423
QY 320 KGSIOKFVPIYLIAGIQHCCODI-GARSLSVLR 351
Db 424 KGFKEIITHQNGGLR-SCMGLTGCAITDELRT 455

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Search completed: September 26, 2002, 08:28:34
Job time: 138 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2002, 08:24:46 : Search time 32.36 Seconds

(without alignments)
1318.057 Million cell updates/sec

Title: US-09-853-918-30

Perfect score: 1955

Sequence: 1 MADYLLSGTGYVEDLTA.....MSAQIEGVTGLHSEKRLY 384

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

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22: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1778.5	91.0	604	22	ABG22269	Novel human diapo
2	1655	84.7	514	11	AAK05431	Chinese hamster IM
3	1653	84.6	514	11	AAK05432	Human IMPDH. Hom
4	1557	79.6	430	22	ABG23731	Novel human diapo
5	1348.5	69.0	537	22	ABG58547	Drosophila melanog
6	1348.5	69.0	537	22	ABG58547	Drosophila melanog
7	1016	52.0	502	21	AAK30888	Arabidopsis thalia
8	1013.5	51.8	503	21	AAK20989	Arabidopsis thalia
9	1007.5	51.5	503	21	AAK43108	Arabidopsis thalia
10	986.5	50.5	371	20	AAV08965	A. gossypii inosin
11	963	49.3	287	22	ABG07490	Novel human diapo

12	886	45.3	443	21	AAK30889	Arabidopsis thalia
13	878.5	44.9	444	21	AAK20990	Arabidopsis thalia
14	872.5	44.6	444	21	AAK43109	Arabidopsis thalia
15	860	44.0	435	21	AAK30890	Arabidopsis thalia
16	852.5	43.6	436	21	AAK20991	Arabidopsis thalia
17	846.5	43.3	436	21	AAK43110	Arabidopsis thalia
18	691.5	35.4	215	22	AAK70679	S cerevisiae apopt
19	677.5	34.7	203	22	ABG22268	Novel human diapo
20	632	32.3	489	22	AAK36360	Pseudomonas aerugi
21	625	32.0	185	21	AAK58731	Breast and ovarian
22	616	31.5	488	22	AAK82607	S. epidermidis ope
23	615	31.5	506	22	AAK90418	C glutamicum prote
24	615	31.5	506	22	AAK80106	Corynebacterium gl
25	605.5	31.0	489	21	AAV97820	Pseudomonas sp. WF
26	600.5	30.7	488	22	AAV29344	Novel mar regulate
27	587.5	30.1	487	21	AAK44532	Virulence gene pro
28	586.5	30.0	488	22	AAK03593	Haemophilus Influe
29	574.5	29.4	492	22	AAK01060	CFE 63 protein seq
30	574	29.4	481	19	AAK98634	H. pylori GHPD 307
31	572	29.3	481	19	AAV11109	H. pylori ORF hp8e
32	528.5	27.0	514	22	AAK58049	Protonibacterium
33	516	26.4	152	21	AAK27200	Zea mays protein f
34	502	25.7	161	21	AAK03970	Human secreted pro
35	491	25.1	485	22	AAK96466	Putative P. abyssi
36	484	24.8	140	21	AAK27201	Zea mays protein f
37	470	24.0	133	21	AAK27202	Zea mays protein f
38	447	22.9	266	20	AAV34772	Chlamydia pneumonia
39	376	19.2	95	22	AAK04552	Human polypeptide
40	362.5	18.5	479	22	AAK04859	Micromonospora eve
41	351.5	18.0	477	22	AAK92691	C glutamicum prote
42	351.5	18.0	477	22	AAK80109	Corynebacterium gl
43	351	18.0	155	22	ABG22266	Novel human diapo
44	351	18.0	217	21	AAK58491	Lung cancer associ
45	345	17.6	348	19	AAK52169	Human MKK3-interac
46	345	17.6	348	22	AAK38661	Human polypeptide
47	345	17.6	348	22	AAK66724	Human dehydrogenas
48	345	17.6	366	19	AAK37945	Amino acid sequenc
49	341	17.4	66	22	ABG22265	Novel human diapo
50	341	17.4	325	22	AAK35218	Enterococcus faeca
51	341	17.4	327	22	AAK33399	Enterococcus faeca
52	339	17.3	325	22	AAK35850	Helicobacter pylori
53	333.5	17.1	151	20	AAV08964	A. gossypii inosin
54	331.5	17.0	328	22	AAK37668	Streptococcus pneu
55	331.5	17.0	447	22	AAK40447	Human polypeptide
56	327.5	16.8	447	22	AAK40448	Human polypeptide
57	326.5	16.7	409	22	AAK38662	Human polypeptide
58	317	16.2	347	22	AAK34442	E. coli cellular p
59	312	16.0	325	22	AAK83101	S. epidermidis ope
60	307	15.7	350	21	AAV93154	Human guanosine mo
61	295	15.1	325	22	AAU37145	Staphylococcus aur
62	295	15.1	325	22	AAU37462	Staphylococcus aur
63	295	15.1	347	22	AAK38321	Salmonella typhi c
64	290	14.8	156	22	ABG22267	Novel human diapo
65	289.5	14.8	471	22	AAK45471	Protonibacterium
66	282	14.4	55	22	AAK75199	Human colon cancer
67	263	13.5	220	22	ABG07806	Novel human diapo
68	260	13.3	178	22	AAK80108	Corynebacterium gl
69	256.5	13.1	732	22	ABG30033	Novel human diapo
70	215	11.0	174	22	AAK82455	S. epidermidis ope
71	209.5	10.7	359	22	ABG07805	Novel human diapo
72	208	10.6	158	22	AAK80107	Corynebacterium gl
73	192.5	9.8	378	22	AAK58050	Protonibacterium
74	190.5	9.7	265	21	AAK56994	Human prostate can
75	190.5	9.7	292	22	AAU23259	Novel human enzyme
76	190.5	9.7	292	22	AAK43631	Human polypeptide
77	190.5	9.7	292	22	AAU21663	Human polypeptide
78	179	9.2	87	20	AAV35423	Novel human neopla
79	179	9.2	374	22	AAK90420	Chlamydia pneumonia
80	161	8.2	374	22	AAK90420	C glutamicum prote
81	161	8.2	401	22	AAK80117	Corynebacterium gl
82	127	6.7	401	22	AAK38235	Salmonella typhi c
83	126	6.5	324	22	AAE02209	Streptococcus pneu
84	125	6.4	79	21	AAK02568	Human secreted pro
			324	22	AAK02568	CFE 9 protein sequ

Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
S cerevisiae apopt
Novel human diapo
Pseudomonas aerugi
Breast and ovarian
S. epidermidis ope
C glutamicum prote
Corynebacterium gl
Pseudomonas sp. WF
Novel mar regulate
Virulence gene pro
Haemophilus Influe
CFE 63 protein seq
H. pylori GHPD 307
H. pylori ORF hp8e
Protonibacterium
Zea mays protein f
Human secreted pro
Putative P. abyssi
Zea mays protein f
Zea mays protein f
Chlamydia pneumonia
Human polypeptide
Micromonospora eve
C glutamicum prote
Corynebacterium gl
Novel human diapo
Lung cancer associ
Human MKK3-interac
Human polypeptide
Human dehydrogenas
Amino acid sequenc
Novel human diapo
Enterococcus faeca
Enterococcus faeca
Helicobacter pylori
A. gossypii inosin
Streptococcus pneu
Human polypeptide
Human polypeptide
Human polypeptide
E. coli cellular p
S. epidermidis ope
Human guanosine mo
Staphylococcus aur
Staphylococcus aur
Salmonella typhi c
Novel human diapo
Protonibacterium
Human colon cancer
Novel human diapo
Corynebacterium gl
Novel human diapo
S. epidermidis ope
Novel human diapo
Corynebacterium gl
Protonibacterium
Human prostate can
Novel human enzyme
Human polypeptide
Human polypeptide
Novel human neopla
Chlamydia pneumonia
C glutamicum prote
Corynebacterium gl
Salmonella typhi c
Salmonella typhi c
Streptococcus pneu
Human secreted pro
CFE 9 protein sequ

85 124 6.3 324 22 AAU37766 Streptococcus pneu
86 117 6.0 318 22 AAU53326 Enterococcus faeca
87 116.5 6.0 221 AAG27445 Arabidopsis thalia
88 116.5 6.0 255 21 AAG37444 Arabidopsis thalia
89 116.5 6.0 260 21 AAG37443 Arabidopsis thalia
90 116.5 6.0 312 21 AAG37849 Arabidopsis thalia
91 116.5 6.0 317 21 AAG36985 Arabidopsis thalia
92 116.5 6.0 317 21 AAG53311 Arabidopsis thalia
93 116.5 6.0 338 21 AAG27848 Arabidopsis thalia
94 116.5 6.0 343 21 AAG36984 Arabidopsis thalia
95 116.5 6.0 343 21 AAG53310 Arabidopsis thalia
96 116.5 6.0 358 21 AAG37847 Arabidopsis thalia
97 116.5 6.0 363 21 AAG36983 Arabidopsis thalia
98 116.5 6.0 363 21 AAG53309 Arabidopsis thalia
99 115 5.9 351 22 AAU53391 Pseudomonas aerugi
100 114.5 5.9 333 21 AAG55063 Arabidopsis thalia

ALIGNMENTS

RESULT 1

ABG22269 standard; protein: 604 AA.

AC ABG22269;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #22260.

KM Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN NC200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001MO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.

DR N-PSDB; AAS86456.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

PS Claim 20; SEQ ID NO 52628; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations in

CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pcl_sequences](http://wipo.int/pub/published_pcl_sequences).

XX Sequence 604 AA;

Query Match 91.0%; Score 1778.5; DB 22; Length 604;
Best Local Similarity 71.3%; Pred. No. 1,3e-165;
Matches 367; Conservative 5; Mismatches 12; Indels 131; Gaps 2;

QY 1 MADVLISGNGYVPEDEGTFQAQOLFASADGLTYNDFLLPGFIDFIDEVDLTSALTRKIT 60
DB 90 madylisgngyvpedgltaqqlfasaddltyndflllpgfidfidevdltsaltrkit 149
QY 61 LKTPLISSPMDTVTEADMAIAMLGSGIGFIHNCTPEFQANEVKKVKPKD----- 112
DB 150 lktpliisspmdtvtreadmatamalmngigfihncfpefanevrkvnklegfildpv 209
QY 113 ----- 112
DB 210 lpshtvgdvlegkmrhgfsgipiteltgmsklvgivtsrdidflaekdhtllsevm 269
QY 113 ----- 112
DB 270 prlelvapagvclkeanellgrskkklplvndcdelvaliartdlkserdylpaskds 329
QY 113 --TLGCAAVGTREDDXRYLDLTOAGVDVYLDSSGNSVYQIAMWYTRKXPHLOVI 170
DB 330 qpqlcgaaavtreedkkyridllltqagvdvlydssgnsavyqarvlyefkxphlqv 389
QY 171 GGNVVTAAQAKNLLDAGVDDLRVGMGGSGICITQEWACGRPGT-AVYVAEYARREGV 229
DB 390 ggnvvtaaqaknlldagvddlrvgmgsgslctqevnacgrpgtccvtrxaeartfgy 449
QY 230 PIADGCIQTVGNHVKALALAGASTVMGSLAATTEAPGEYFSDGVRLLKRYGMSIDA 289
DB 450 pilaagdlqtvgnhvkalaagastvmgslaatteapgeyfsdgyrllkrygmgsida 509
QY 290 MEKSSSSQKRTFSEGDYKKAQGVSGSIQDKGSIQKAVPPLIAGIOHCODIGARSLVL 349
DB 510 meksssqkryfsegdvkvkaqgvssiqdkysiqkltvpyllagiqgcqdigarslsvl 569
QY 350 RSMWYSGELKFEKRTMSAOIEGGVGHLSYEKRLY 384
DB 570 rsmwysgelkfekrmspqliegvgvnglnsyekrily 604

RESULT 2

ID AAR05431 standard; protein: 514 AA.

AC AAR05431;

DT 31-AUG-1990 (first entry)

DE Chinese hamster IMPDH.

KW Inosine 5'-mono-phosphate dehydrogenase; hepatomas;

KW guanosine monophosphate.

OS Cricetus sp.

PN W09001545-A.

PD 22-FEB-1990.

PF 02-AUG-1989; 89MO-0000344.

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KW				PR	24-JUN-1999;	990S-0140695
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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Query Match Similarity      43.3%; Score 846.5; DB 21; Length 436;
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Db          301 lvlgsylvmmgsflaagstleaapgyeyetngkrlikkyrgmgsleamekc--gsdqaryldqtlc 358
QY          307 VKIAGVSGSIODKSGISIKFVPLYLLAGIOHGCODDIGARSLSVLIRSMMYSGELKEFEKRTWS 366
||||| :||| :||| :||| :||| :||| :||| :|||
Db          359 lkiaagvyvgavaadksvylklipytmhavkqgfqdligaaslgaahnlrlrleartfya 418
QY          367 AOIEGCVGHLSYEKRKY 384
||||| :||| :||| :||| :||| :||| :||| :|||
```


	Matches	142:	Conservative	6:	Mismatches	11:	Indels	59:	Gaps	2:
QY	76	ADMAIAMAALMGIGIFIHNNCTPEFOANEVKKVKED-----								111
Dd	1	adiataamalmgigifihnnctpefqakevkrkkfeggfildrvlltphstvgdvleakm								60
QY	112	-----KTLICGAAVGTRREDDKIRLDLLTOAGVD								139
Dd	61	rhtgfsghlteleqtlgsalknrdyplaskdsbhkqllrgaaavgtpeddkyrldllltqagvd								120
QY	140	VIVLDSOGNSNYOYFAMVHYIKOKYPHLOVIGANVTVAQAANKLIDAGVDGLRVGMCGS								199
Dd	121	vvlidlsognsnyygatclathylkqkyphlgvis---mtlaeqanlldaaavglrtigmcgs								177
QY	200	ICTIOEVMACGRPOGTAVYKYAEVARRRGPVIADGGI								237
Dd	178	ictitgevmacggpggtalyskaeyalcfcgvsladgsl								215
RESULT	20									
AUJ36360	ID	AUJ36360 standard; Protein: 489 AA.								
XX	AC	AUJ36360;								
XX	DT	14-FEB-2002 (first entry)								
DE	Pseudomonas aeruginosa cellular proliferation protein #350.									
KW	Antisense: prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.									
OS	Pseudomonas aeruginosa.									
PN	WO200170955-A2.									
PD	27-SEP-2001.									
PF	21-MAR-2001; 2001WO-US09180.									
PR	21-MAR-2000; 2000US-191078P. 23-MAY-2000; 2000US-206848P. 26-MAY-2000; 2000US-207272P. 23-OCT-2000; 2000US-242578P. 27-NOV-2000; 2000US-253625P. 22-DEC-2000; 2000US-257931P. 16-FEB-2001; 2001US-269308P.									
PA	(ELIT-) ELITRA PHARM INC.									
P1	Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr CJ;									
P1	Yamamoto RT, Xu HH;									
DR	WPJ: 2001-6111495/770. N-PSTDB; AAS54219.									
PT	New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids - Example 3; Seq ID No 11953; 51pp; English.									
CC	The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen									

CC	for homologous nucleic acids which are required for cell proliferation in
CC	a wide variety of organisms. The present sequence represents an
CC	essential prokaryotic cellular proliferation protein.
CC	Note: The sequence data for this patent did not form part
CC	of the printed specification, but was obtained in electronic
CC	format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences.
XX	
XX	Sequence 489 AA:
XX	
XX	Query Match 32.3%; Score 632; DB 22; Length 489:
XX	Best Local Similarity 33.4%; Pred. No. 3,6e-53;
XX	Matches 159; Conservative 55; Mismatches 130; Indels 132; Gaps 4
OY	26 SADIATYNDLFILPGFIDFIADVDLTSLATKTLTKPFLISSPMDYTEADMAIAML 85
DB	5 Sgealttdvlllpdysevlpkdvskltltlgieinlpvsaandvtlearialamag 64
OY	86 GGIGFIHHNCTPERFQANVRKRPD----- 111
DB	65 ggigilnhkmngieqgaevrkvkkhetalvrdpvtvtpstkliellqmareygsfgfpv 124
OY	112 ----- 111
DB	125 eggelvgvltvgrdlrvkknagdtvaaimprkklvtaregrpleemkaklyenrlekm 184
OY	112 -----KT-----LLCGAAGTREDDKYRLDLLTQAGVDVI 141
DB	185 vdenfylvrlgtvftfdlaktvplaakdegrllrygaavgradrgervaaalvaagv 244
OY	142 VLDSSQGNSTQYIAMVHYIKQKYPHLOVIGNVTAAQKNLIDAGVDGLRYGMCSSIC 201
DB	245 vvdltahbskgylerlvrvwqtfprdvvgignataeakaalaeagadvkvgiypgsic 304
OY	202 ITQEVMAAGRRGQTAAYVKNVAEYARRRCVPIADCGIQTYGNHYKALAGASTVMMSGL 261
DB	305 fltrivagvypqisaalanaalegrtgvpladaggrlrfisgdakamvgaeyvmmgsma 364
OY	262 ATTAPAGEYFFSDVRLLKRRGMSGLDAMEKSSSSQKRFF---SEGDDVKIKIQVSGSIQ 318
DB	365 gteepgeielfgtryksyrgmgslygamsggysgdsdryfdgasagaelvpegielgrv 424
OY	319 DKGSITQKFPYLLAGIQHGCODIGANSLSVLRSMYSGELKREKRTMSAQLBGGVH 374
DB	425 ykgalsalvbnqlmgglraamgytgsadiqmnt-----qpqfvrlitlgagmaeshv 475
XX	
XX	RESULT 21
XX	ID AAB58731
XX	AAB58731 standard; Protein; 185 AA.
XX	AAB58731;
XX	
XX	27-MAR-2001 (first entry)
XX	
XX	Breast and ovarian cancer associated antigen protein sequence SEQ ID 439.
XX	
XX	Human; breast cancer; ovarian cancer; cytosolic; immunosuppressive;
XX	nootropic; neuroprotective; antiviral; antileukemic; hepatotropic;
XX	antidiabetic; antiinflammatory; antifungal; vulnery; anticonvulsant;
XX	antibacterial; antifungal; antiparasitic; cardiac; immune disorder;
XX	Addison's disease; allergy; autoimmune hemolytic anemia;
XX	autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
XX	multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
XX	cardiovascular disorder; wound healing; neurological disease.
XX	
XX	Homo sapiens.
XX	
XX	WO20005173-A1.
XX	
XX	21-SEP-2000.

DB 369 teesppatevfqgrgkyvrygmstlgamekgsnd--ryfge-dkprkfvpeglegrtay 425
 OY 320 KSSIOKFVYLLAGIOHGCODIGARSLVLRSMVSGELKFEKFRMTSAQIEGSHL 376
 DB 426 kbpilgtllylmgvragmytcsenlkkhlfre-----eaqflrmgpaiaeshphnv 477

RESULT 23

AAG90418
 ID AAG90418 standard; Protein; 506 AA.

AC AAG90418;

DT 26-SEP-2001 (first entry)

DE C glutamicum protein fragment SEQ ID NO: 4172.

KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;

KM organic acid synthesis.

OS Corynebacterium glutamicum.

PN EP1108790-A2.

PD 20-JUN-2001.

PF 18-DEC-2000; 2000EP-0127688.

PR 16-DEC-1999; 99JP-0377484.

PR 07-APR-2000; 2000JP-0159162.

PR 03-AUG-2000; 2000JP-0280988.

PA (KYOW) KYOWA HAKKO KOGYO KK.

PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;

PI Tateishi N, Senoh A, Ikeda M, Ozaki A;

DR MPI: 2001-376931/40.

DR N-PSDB; AAH65637.

PT Novel polynucleotides derived from Coryneform bacteria, for identifying

PT mutation point of a gene, measuring expression of a gene, analysing

PT expression profile or pattern of a gene and identifying homologous gene

PS Claim 17: SEQ ID NO: 4172; 246bp + Sequence Listing; English.

CC The present invention provides a number of nucleotide and protein

CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These

CC are useful for identifying the mutation point of a gene derived from a

CC mutant of coryneform bacterium, measuring expression amount and

CC analysing the expression profile or expression pattern of a gene derived

CC from Coryneform bacterium, and identifying a homologue of a gene derived

CC from coryneform bacterium. Coryneform bacteria are useful for producing

CC amino acids, nucleic acids, vitamins, saccharides and organic acids,

CC particularly L-lysine. The present sequence is a protein described

CC in the exemplification of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from the

CC European Patent Office.

CC Sequence 506 AA:

Query Match 31.5%; Score 615; DB 22; Length 506;

Best Local Similarity 32.2%; Pred. No. 1.8e-51;

Matches 148; Conservative 63; Mismatches 115; Indels 134; Gaps 6;

OY 29 GLVYNPLIGRIFIDPDEVDTLSALTRKITKTPLISSPMQVTEADAIMALMGCT 88

DB 21 gltiddvlllpdasdvpsvdstqltrnrlntpllsamdtvleaamaigmartg91 80

OY 89 GFTHN-----CTPE----- 98

DB 81 gvlhnlslsqeaaenvelvkrsesgmvtidpvtctpdmsiqevddlcarfleglpvdea 140

OY 99 -----FOANEVRK----- 106

DB 141 gklvgictnrnhrfeesdmrrvaevmtmpmlvvaeevltkegalalllsankvcklpliak 200

OY 107 -----VKREDKT-----LLGAAVGTREDDKYRDLTLTGAVDPIYVD 144

DB 201 dgklvglltvdktfvkteqpnaskdasgrllvaagigtgeesfragaaladagvdllyvd 260

OY 145 SSGNSVQIAMVHYIKORYPHLOVIGNVVTAQAOKNLIDAGVDELRYMGCGSICITQ 204

DB 261 sahabergvldmvsrvkksfepkvdvlglnlatreaaqlleaadaikvlgisicttr 320

OY 205 EVMACGRPGGTAVYKAEARRFVPIINDGGIQTGYGVKALALGASIVMGSLLAAT 264

DB 321 vvaqvgapqitameaavpahkayplladgymqfsgdlakalaagansvmlsmlagta 380

OY 265 EAPGEYFSDGYRLKKYRGMSLDAM-----EKSSSOKRYFSEGDVK--IAQVGS 314

DB 381 eapgetitngkykryrgmngamgrglsgekrtsykdryfgsdvksedklypegie 440

OY 315 GSIDKGSIQKFPYLLAGIOHGCODIGARSLVLRSMV 354

DB 441 grvfrgplgdllhgvvgglraamygtssltleelnarf 480

RESULT 24

AAB80106
 ID AAB80106 standard; Protein; 506 AA.

AC AAB80106;

DT 30-APR-2001 (first entry)

DE Corynebacterium glutamicum MP protein sequence SEQ ID NO:946.

KW Corynebacterium glutamicum; metabolic pathway protein; MP protein;

KW fine chemical production; microorganism; organic acid; nucleotide;

KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;

KW lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;

KW carbohydrate; aromatic compound; cofactor; polyketide; enzyme.

OS Corynebacterium glutamicum.

PN WO200100843-A2.

PD 04-JAN-2001.

PF 23-JUN-2000; 2000WO-IB00923.

PR 25-JUN-1999; 99US-0141031.

PR 01-JUL-1999; 99DE-1030476.

PR 02-JUL-1999; 99US-0142101.

PR 08-JUL-1999; 99DE-1031415.

PR 08-JUL-1999; 99DE-1031418.

PR 08-JUL-1999; 99DE-1031419.

PR 08-JUL-1999; 99DE-1031420.

PR 08-JUL-1999; 99DE-1031424.

PR 08-JUL-1999; 99DE-1031428.

PR 08-JUL-1999; 99DE-1031434.

PR 08-JUL-1999; 99DE-1031435.

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PR 08-JUL-1999; 99DE-1031632.
PR 08-JUL-1999; 99DE-1031634.
PR 08-JUL-1999; 99DE-1031636.
PR 05-JUL-1999; 99DE-1032125.
PR 05-JUL-1999; 99DE-1032126.
PR 05-JUL-1999; 99DE-1032130.
PR 05-JUL-1999; 99DE-1032186.
PR 09-JUL-1999; 99DE-1032206.
PR 09-JUL-1999; 99DE-1032227.
PR 09-JUL-1999; 99DE-1032228.
PR 09-JUL-1999; 99DE-1032229.
PR 09-JUL-1999; 99DE-1032230.
PR 14-JUL-1999; 99DE-1032922.
PR 14-JUL-1999; 99DE-1032926.
PR 14-JUL-1999; 99DE-1032928.
PR 14-JUL-1999; 99DE-1033004.
PR 14-JUL-1999; 99DE-1033005.
PR 14-JUL-1999; 99DE-1033006.
PR 12-AUG-1999; 99US-0148613.
PR 27-AUG-1999; 99DE-1040764.
PR 27-AUG-1999; 99DE-1040765.
PR 27-AUG-1999; 99DE-1040766.
PR 27-AUG-1999; 99DE-1040832.
PR 31-AUG-1999; 99DE-1041378.
PR 31-AUG-1999; 99DE-1041379.
PR 31-AUG-1999; 99DE-1041380.
PR 31-AUG-1999; 99DE-1041394.
PR 31-AUG-1999; 99DE-1041396.
PR 03-SEP-1999; 99DE-1042076.
PR 03-SEP-1999; 99DE-1042077.
PR 03-SEP-1999; 99DE-1042079.
PR 03-SEP-1999; 99DE-1042086.
PR 03-SEP-1999; 99DE-1042087.
PR 03-SEP-1999; 99DE-1042088.
PR 03-SEP-1999; 99DE-1042095.
PR 03-SEP-1999; 99DE-1042124.
PR 03-SEP-1999; 99DE-1042129.
PR 09-MAR-2000; 2000US-0187970.
XX
XX (BAD1 ) BASF AG.
XX
XX Pompejus M, Kroegeer B, Schroeder H, Zelder O, Haberhauer G;
XX
XX WPI: 2001-137957/14.
XX
XX DR N-PSDB; AAF72225.
XX
XX Nucleic acids from Corynebacterium glutamicum encoding metabolic
XX PT pathway proteins, useful for producing fine chemicals in
XX PT microorganisms, including organic acids, nonproteinogenic amino acids,
XX PT and purine and pyrimidine bases -
XX
XX Claim 20; Page 1451-1452; 1737PP; English.
XX
XX AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic
XX CC pathway (MP) proteins given in AAB7634 to AAB80211. The C. glutamicum
XX CC MP nucleic acids are useful for the production of fine chemicals
XX CC in microorganisms, including organic acids, nonproteinogenic amino
XX CC acids, purine and pyrimidine bases, nucleosides, lipids,
XX CC saturated and unsaturated fatty acids, diols, carboxylates, aromatic
XX CC compounds, vitamins, cofactors, polyketides and enzymes.
XX
XX Sequence 506 AA;
SQ
Query Match 31.5%; Score 615; DB 22; Length 506;
Best Local Similarity 32.2%; Pred. No. 1.8e-51;
Matches 148; Conservative 63; Mismatches 115; Indels 134; Gaps 6;
QY 29 GLTYNDFLLPGFIDFADEVLTSAITRKITTKPLISSPMDTVTEADMAIAMALMGGI 88
Db 21 gltfdvlllpdsadvpsevdtsqtrlnrlntpllsamdtvtsearnaigmargyi 80
QY 89 GFTHHN-----CTPE----- 98
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Db 81 gvlhnrnsiqeaeenvelvkrsesgmvltpvtctpdmisqevddlcarfrisqjpvvdea 140
QY 99 -----EQANEVRK----- 106
Db 141 gklvgictnrdmrfesdmnrvaewtcmpllvaaegvvtkegalalisanhveklpila 200
QY 107 -----VKKFDKT-----LLCGAAVGTREDDKYRLDLLTQAGVDVITLD 144
Db 201 dgklvglltvtkdfvkteqhpnskaasgrlllvaagistgesfrragalaadagvdlivvd 260
QY 145 SSQGNSTVYQIAMVHYITQKPHLOVIGCNVYTAQAANLIDAGVDGRLVNGCGSITITQ 204
Db 261 sahsrgrvldmvsrvkksfpkvdvlgnglatreaagameaadaikvqjippsicltr 320
QY 205 EVMACGRPGTAAVKKVVAEVARFEPITADGIGTQVHHVVKALALGASTVMMGSLAATP 264
Db 321 vvaagvgaqqltalameaavpahkagvplladgmgfsgdikaalaagansvmlsmlagta 380
QY 265 EAPGEYFSDGVRLKXKRGMSLDAM-----EKSSSSQKRYFSEGDYKVK---IAQGV 314
Db 381 eaqpetltngkykrytgmngmgmrglsgkexskdryfygsdvksecklvpegie 440
QY 315 GSIDKGSIGKFPVYLLAGIQHGCQDIGARSLSVLRSMRY 354
Db 441 gvpftrpigdilhqvgyglraamytcgsstleelhnarf 480
RESULT 25
AAV97820
ID AAV97820 standard; Protein; 489 AA.
XX
XX AAV97820;
AC
XX 29-AUG-2000 (first entry)
DT
XX
XX Pseudomonas sp. WP505 ORF6-3 protein, SEQ ID NO:5.
DE
XX
XX Benzothioephene oxidase; bto gene cluster; desulphurisation; crude oil;
XX KW decontamination.
XX
XX Pseudomonas sp. WP505.
OS
XX
XX JP2000093180-A.
PN
XX
XX 04-APR-2000.
PD
XX
XX 28-SEP-1998; 98UP-0272744.
PF
XX
XX 28-SEP-1998; 98UP-0272744.
PR
XX
XX (TOFU ) TONEN CORP.
PA
XX
XX WPI: 2000-378972/33.
XX DR N-PSDB; AAA38391.
XX
XX New proteins useful for desulfurization of crude oil have ability to
XX PT control expression of benzothioephene oxidase group -
XX
XX Example 1; Page 19-20; 43pp; Japanese.
XX
XX The invention relates to proteins encoded by the benzothioephene oxidase
XX CC (bto) gene cluster from Pseudomonas sp. WP505, specifically the protein
XX CC which controls expression of the gene cluster (AAV97827), the
XX CC benzothioephene oxidase (bto) enzyme itself (AAV97825) and a
XX CC benzothioephene oxidase co-enzyme (AAV97824), which controls
XX CC benzothioephene activity via redox regulation. These enzymes are
XX CC respectively encoded by the bto gene cluster open reading frames ORF2-16
XX CC (AAA38398), ORF4-9 (AAA38396) and ORF6-7 (AAA38395). The invention also
XX CC encompasses genetic constructs and vectors comprising the genes encoding
XX CC these proteins, hosts containing such constructs and the recombinant
XX CC production of the enzymes. Pseudomonas sp. WP505 benzothioephene oxidase,
XX CC benzothioephene oxidase co-enzyme and bto gene cluster regulator are
```


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OM protein - protein search, using sw model

Run on: September 26, 2002, 08:25:06 ; Search time 12.98 Seconds
(without alignments)
722.606 Million cell updates/sec

Title: US-09-853-918-30

Perfect score: 1955
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Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Issued_Patents_AA:*
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5: /cgn2_6/ptodata/2/1aa/PTOUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1655	84.7	514	4	US-08-925-230-8
2	1653	84.6	514	4	US-08-925-230-7
3	345	17.6	366	1	US-08-774-169-1
4	341	17.4	345	1	US-08-774-169-4
5	306.5	15.7	346	1	US-08-774-169-3
6	103	5.3	374	1	US-08-625-876-2
7	100	5.1	374	1	US-08-625-876-4
8	99	5.1	374	1	US-08-625-876-6
9	95	4.9	369	1	US-08-253-823-1
10	95	4.9	369	1	US-08-290-508-3
11	95	4.9	369	2	US-08-606-144-1
12	95	4.9	369	2	PCT-US94-02174-3
13	94.5	4.8	448	1	US-08-074-121-3
14	94.5	4.8	448	1	PCT-US94-06447-3
15	93.5	4.8	593	2	US-08-591-079-8
16	93.5	4.8	593	2	US-08-591-079-10
17	91.5	4.7	441	1	US-08-403-866-10
18	91	4.7	1052	4	US-09-255-502-7
19	90	4.6	2314	4	US-09-268-347-49
20	88	4.5	745	1	US-08-453-472-5
21	88	4.5	745	1	US-08-038-948-9
22	88	4.5	745	1	US-08-453-952-5
23	88	4.5	745	2	US-08-484-993B-43
24	88	4.5	745	2	US-08-862-903-5
25	88	4.5	745	2	US-08-484-158B-43
26	88	4.5	745	2	US-08-484-158A-43
27	88	4.5	745	2	US-08-480-150A-43

28	88	4.5	745	3	US-08-458-731-43	Sequence 43, Appl
29	88	4.5	745	3	US-08-149-223A-43	Sequence 43, Appl
30	87.5	4.5	1025	2	US-08-304-309-2	Sequence 2, Appl
31	87.5	4.5	1025	3	US-08-991-942-2	Sequence 2, Appl
32	87.5	4.5	1025	5	US-09-138-103-2	Sequence 4, Appl
33	87.5	4.5	1025	5	PCT-US95-04567-4	Sequence 4, Appl
34	86	4.4	251	2	US-08-846-762-11	Sequence 11, Appl
35	86	4.4	956	3	US-08-772-270A-8	Sequence 8, Appl
36	85.5	4.4	413	3	US-08-977-001-3	Sequence 3, Appl
37	85.5	4.4	682	1	US-08-441-139-2	Sequence 2, Appl
38	85.5	4.4	713	1	US-08-188-228-62	Sequence 62, Appl
39	85.5	4.4	713	1	US-08-332-643-56	Sequence 56, Appl
40	85.5	4.4	713	1	US-08-332-638-62	Sequence 62, Appl
41	85	4.3	323	6	5185254-4	Patent No. 5185254
42	84	4.3	1713	3	US-08-600-982-24	Sequence 24, Appl
43	84	4.3	1713	3	PCT-US94-10261A-24	Sequence 24, Appl
44	84	4.3	2511	4	US-09-261-907-2	Sequence 2, Appl
45	82	4.2	434	1	US-08-404-127-2	Sequence 2, Appl
46	82	4.2	434	2	US-09-041-011-2	Sequence 2, Appl
47	82	4.2	444	3	US-09-221-235-14	Sequence 14, Appl
48	82	4.2	444	3	US-09-221-928-14	Sequence 14, Appl
49	82	4.2	444	4	US-09-221-527-14	Sequence 14, Appl
50	82	4.2	444	4	US-09-221-236-14	Sequence 14, Appl
51	82	4.2	444	4	US-09-221-416-14	Sequence 14, Appl
52	82	4.2	444	4	US-09-221-245-14	Sequence 14, Appl
53	82	4.2	444	4	US-09-163-115-14	Sequence 14, Appl
54	82	4.2	444	4	US-09-221-528-14	Sequence 14, Appl
55	82	4.2	444	4	US-09-593-553-14	Sequence 14, Appl
56	82	4.2	444	4	US-09-221-237-14	Sequence 14, Appl
57	82	4.2	444	1	US-08-404-127-4	Sequence 4, Appl
58	82	4.2	445	2	US-09-041-011-4	Sequence 4, Appl
59	82	4.2	529	2	US-08-933-227-4	Sequence 4, Appl
60	82	4.2	540	2	US-08-368-834-20	Sequence 20, Appl
61	82	4.2	541	2	US-08-467-822-34	Sequence 34, Appl
62	82	4.2	541	2	US-08-447-154-19	Sequence 19, Appl
63	82	4.2	541	4	US-08-432-697-34	Sequence 34, Appl
64	82	4.2	541	4	US-08-466-248-34	Sequence 34, Appl
65	82	4.2	1360	4	US-09-393-259-2	Sequence 2, Appl
66	82	4.2	2509	1	US-08-466-005A-10	Sequence 10, Appl
67	81	4.1	423	2	US-08-715-554-2	Sequence 2, Appl
68	81	4.1	423	2	US-08-583-118-2	Sequence 2, Appl
69	80.5	4.1	456	2	US-08-679-635A-6	Sequence 6, Appl
70	80.5	4.1	341	1	US-08-314-309A-19	Sequence 19, Appl
71	80.5	4.1	524	3	US-08-557-210A-3	Sequence 3, Appl
72	80.5	4.1	539	3	US-08-557-210A-5	Sequence 5, Appl
73	80.5	4.1	539	3	US-08-348-353-17	Sequence 17, Appl
74	80.5	4.1	1248	2	US-08-465-965-17	Sequence 17, Appl
75	80.5	4.1	1248	2	US-08-465-966-17	Sequence 17, Appl
76	80.5	4.1	1248	2	US-08-465-966-17	Patent No. 5472855
77	80	4.1	275	6	US-08-431-387-7	Sequence 7, Appl
78	80	4.1	276	1	US-08-361-611-4	Sequence 4, Appl
79	80	4.1	484	1	US-08-565-655-4	Sequence 4, Appl
80	80	4.1	484	2	US-08-946-967-4	Sequence 4, Appl
81	80	4.1	484	2	US-08-946-967-4	Sequence 4, Appl
82	80	4.1	691	5	PCT-US91-08442-2	Sequence 2, Appl
83	79.5	4.1	641	4	US-08-836-567-10	Sequence 10, Appl
84	79.5	4.1	3782	4	US-09-105-537-4	Sequence 4, Appl
85	79	4.0	275	5	PCT-US93-00418-3	Sequence 3, Appl
86	79	4.0	432	4	US-09-282-305-10	Sequence 10, Appl
87	79	4.0	947	4	US-09-228-986-73	Sequence 73, Appl
88	78.5	4.0	274	1	US-08-431-387-2	Sequence 2, Appl
89	78.5	4.0	274	2	US-08-865-203-7	Sequence 7, Appl
90	78.5	4.0	274	2	US-07-849-420-7	Sequence 7, Appl
91	78.5	4.0	274	4	US-09-253-854-7	Sequence 7, Appl
92	78.5	4.0	274	4	US-08-955-424-7	Sequence 7, Appl
93	78.5	4.0	350	1	US-07-923-260A-4	Sequence 4, Appl
94	78.5	4.0	375	1	US-08-121-714-5	Sequence 5, Appl
95	78.5	4.0	375	1	US-08-477-108A-5	Sequence 5, Appl
96	78.5	4.0	375	2	US-08-477-112-5	Sequence 5, Appl
97	78.5	4.0	375	2	PCT-US93-08332-5	Sequence 5, Appl
98	78.5	4.0	378	1	US-07-772-087-4	Sequence 4, Appl
99	78.5	4.0	379	2	US-08-845-295A-1	Sequence 1, Appl
100	78.5	4.0	379	3	US-09-140-933-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-08-925-230-8

; Sequence 8, Application US/08925230

; Patent No. 6147194

; GENERAL INFORMATION:

; APPLICANT: Collart, Frank

; APPLICANT: Huberman, Eliezer

; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO IMPDH

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/925,230

; FILING DATE: September 8, 1997

; CLASSIFICATION: 536

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 5,665,583

; FILING DATE: 12-AUG-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Wilson, Mark B.

; REGISTRATION NUMBER: 37,259

; REFERENCE/DOCKET NUMBER: ARCD:274

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (512) 418-3000

; TELEFAX: (512) 474-7577

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 514 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; US-08-925-230-8

Query Match 84.7%; Score 1655; DB 4; Length 514;

Best Local Similarity 63.6%; Pred. No. 2.6e-171;

Matches 327; Conservative 31; Mismatches 26; Indels 130; Gaps 1;

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QY 1 MADYLLISGGGYPEDELTAQOLFPASADGLTYNDFILDPGFIADAEVLTSLTRKIT 60
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 1 MADYLLISGGGYPEDELTAQOLFPNCGDGLTYNDFILPGYIDFTADQVLTSLTRKIT 60
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 61 LKTPILSSPMDYTEADMAIAMLGIGFIHNCTPEFOANEVRKVKKFD----- 111
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 61 LKTPILSSPMDYTEADMAIAMLGIGFIHNCTPEFOANEVRKVKKFD----- 111
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 112 ----- 111
Db 121 LSPKRDYRVFEAKRHGFCGIPITDTGRMSRLVGISSRDIDFLKEEHRDLFEIIMT 180
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 112 ----- 111
Db 181 KREDLVVAPAGITLKEANELLQSKRGKLPIVENDELVAIIARTDLKKNRDYPLASKDA 240
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 112 -KRLGGAAGTREDKRYRLDLTQAGVDVIVLSSQSGNSVYQIAWHYKOKYPHLOVI 170
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 241 KKOLLGGAIGTHEDKRYRLDLALAGVDVIVLSSQSGNSIFQIIMIKIKKXPENLOVI 300
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
```

```
QY 171 GGNVYTAQAQKNLIDAGVDGLRVMGCGSICITQEVWACGRPGCTAVYKVAEYARRFCVP 230
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 301 GGNVYTAQAQKNLIDAGVDALRVMGCGSICITQEVWACGRPGCTAVYKVAEYARRFCVP 360
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 231 IADGGIQNVGHVVKALALGASTVMGSLAATTEAPGEYFSDGYRLKRYRGMGSLDAM 290
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 361 IADGGIQNVGHVVKALALGASTVMGSLAATTEAPGEYFSDGYRLKRYRGMGSLDAM 420
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 291 EKSSSQRRYSEGDYKRYIAQVSGSIQDKSIOKEFVYLIAGIOHCGODIGARSLSVLR 350
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 421 DKHLSSQNRYSFSEADKRYIAQVSGAVQDKGSIHKFPYLIAGIOHCGODIGARSLSVLR 480
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 351 SMWYSGELKFKRRTMSAQIEGVGHSHYKRLY 384
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 481 AMWYSGELKFKRRTSSNOVGVGHSHYKRLY 514
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
```

RESULT 2

US-08-925-230-7

; Sequence 7, Application US/08925230

; Patent No. 6147194

; GENERAL INFORMATION:

; APPLICANT: Collart, Frank

; APPLICANT: Huberman, Eliezer

; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO IMPDH

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/925,230

; FILING DATE: September 8, 1997

; CLASSIFICATION: 536

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 5,665,583

; FILING DATE: 12-AUG-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Wilson, Mark B.

; REGISTRATION NUMBER: 37,259

; REFERENCE/DOCKET NUMBER: ARCD:274

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (512) 418-3000

; TELEFAX: (512) 474-7577

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 514 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; US-08-925-230-7

Query Match 84.6%; Score 1653; DB 4; Length 514;

Best Local Similarity 63.8%; Pred. No. 4.3e-171;

Matches 328; Conservative 29; Mismatches 27; Indels 130; Gaps 1;

```
QY 1 MADYLLISGGTYPEDELTAQOLFPASADGLTYNDFILDPGFIADAEVLTSLTRKIT 60
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 1 MADYLLISGGTYPEDELTAQOLFPNCGDGLTYNDFILPGYIDFTADQVLTSLTRKIT 60
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 61 LKTPILSSPMDYTEADMAIAMLGIGFIHNCTPEFOANEVRKVKKFD----- 111
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
```

```

Db 61 LKPLVSSPMDTVEAGAAIAAMALTGIGFIHNNCTPEEQANEVRKVKYEGGTTDPVY 120
Qy 112 ----- 111
Db 121 LSPKRVAVDFEAKARHGFCCGIPITDTGRMSRLVGIISRRIDFLKEEHDCFLIEIMT 180
Qy 112 ----- 111
Db 181 KREDLVAPRSITLKEANEILLQRSKKGLPIVNEDELVAIARTDLKKNRDYPLASKDA 240
Qy 112 ----- 111
Db 112 -KTLGCAVGTREDDKRLDLITAGVDYIVLDSOGNSVQIAMHYIKQKTYHLOYI 170
Db 241 KKQLGCAIGITHEDDKRLDLAAGVDVYVLLDSSQNSLFIQIMKIKYKYNLOYI 300
Qy 171 GGNVYTAQAOKNLIDAGVDGLRVGCGSSICTOEWMAAGRPQGTAVYKVAEYARFQV 230
Db 301 GGNVYTAQAOKNLIDAGVDALRVGCGSSICTOEVLAGRQATAVYKVSAYARFQV 360
Qy 231 IADGGIQTGVHVKALALGASTVMGSLLAATTEAPGEYFFSDGVRLLKRYMGSLDM 290
Db 361 VYADGIGNVGHIAKALALGASTVMGSLLAATTEAPGEYFFSDGIRLLKRYMGSLDM 420
Qy 291 EKSSSOKRPFSEGDVKVIAQVSGSIQDQKSIQKFPYLLINGIQHCODIGARSLSVLR 350
Db 421 DKHLSSQNRKYEADKIKVAVGSGAVQDKSIHKFVYLLAGIQHSCODIGAKSLTOVR 480
Qy 351 SMYSGELKFEKRTMSAOIEGGVHGLHSEKRLY 384
Db 481 AMMYSGELKFEKRTMSAOIEGGVHGLHSEKRLY 514

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```

RESULT 3
US-08-774-169-1
; Sequence 1, Application US/08774169
; Patent No. 5756332

```

```

GENERAL INFORMATION:

```

```

APPLICANT: Hillman, Jennifer L.

```

```

TITLE OF INVENTION: A NOVEL GUANOSINE MONOPHOSPHATE REDUCTASE

```

```

NUMBER OF SEQUENCES: 4

```

```

CORRESPONDENCE ADDRESS:

```

```

STREET: 3174 Porter Drive

```

```

CITY: Palo Alto

```

```

STATE: CA

```

```

COUNTRY: USA

```

```

ZIP: 94304

```

```

COMPUTER READABLE FORM:

```

```

MEDIUM TYPE: Diskette

```

```

COMPUTER: IBM Compatible

```

```

OPERATING SYSTEM: DOS

```

```

SOFTWARE: FASTSEQ for Windows Version 2.0

```

```

CURRENT APPLICATION DATA:

```

```

APPLICATION NUMBER: US/08/774.169

```

```

FILING DATE: Herewith

```

```

CLASSIFICATION: 530

```

```

PRIOR APPLICATION DATA:

```

```

APPLICATION NUMBER:

```

```

ATTORNEY/AGENT INFORMATION:

```

```

NAME: Billings, Lucy J.

```

```

REGISTRATION NUMBER: 36,749

```

```

REFERENCE/DOCKET NUMBER: PF-0182 US

```

```

TELECOMMUNICATION INFORMATION:

```

```

TELEPHONE: 415-855-0555

```

```

TELEFAX: 415-845-4166

```

```

TELEX:

```

```

INFORMATION FOR SEQ ID NO: 1:

```

```

SEQUENCE CHARACTERISTICS:

```

```

LENGTH: 366 amino acids

```

```

TYPE: amino acid

```

```

STRANDEDNESS: single

```

```

TOPOLOGY: linear

```

```

IMMEDIATE SOURCE:

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; LIBRARY: Consensus
; CLONE: Consensus
; US-08-774-169-1

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Query Match 17.6%; Score 345; DB 1; Length 366;
Best Local Similarity 29.3%; Pred. No. 4.4e-29;
Matches 97; Conservative 65; Mismatches 145; Indels 24; Gaps 6;

```

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Qy 30 LTYNDFLLPGTDFIA-DEVDTLSALTRKITLKT-----PLISSPMDTVEAGAAIAAMAL 84
Db 28 LDFKVLRLPRKSTLKSSEVDLTRSFERNKQTYSGVPIIAAMDPVATGFEAKVLYCK 87
Qy 85 MGIGFIHNNCT----PEQANEVRKVKFKDITLGAAGVGTREDDKRLDLITQOA--GV 138
Db 88 FSLFATVAKHYLVOMQEFAGNPDCLHEL-----MASSGSSGDFPLEBILIAITQY 141
Qy 139 DVIYLDSSQNSVQIAMHYIKQYPHLOVIGVNVYTAQAOKNLIDAGVDGLRVGCGG 198
Db 142 KYICLDVANGVSEHVEFEVKDKRRFPQHTIMAGVNVYTGEMVEEDILSGADIIVKIGIPG 201
Qy 199 SICITQEWYACGRPGGTAVYKVAEYARRGVPIIADGGIQTGVHVKALALGASTVMGGS 258
Db 202 SVCTTRKKTGVGYPOLSAVMECADAHLKGIHISDGCSCPGDVAKAFAGAGADVMTLGG 261
Qy 259 LLAATTEAPGEYFFSDGVRLLKRYRGMSLDAEKKSSSOKRPFSEGDVKVIAQVSGSIQ 318
Db 262 MLAGHSESGELIENDQKKYKLFYGMSSBMAKKYKAGVAAE-----RASEGKTVEVP 314
Qy 319 DKGSTQKFEVYPIAGIQHSCODIGARSLSVL 349
Db 315 FKGDVEHTRIDILGIRSTCTVYGAAKLKEI 345

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```

RESULT 4
US-08-774-169-4
; Sequence 4, Application US/08774169
; Patent No. 5756332

```

```

GENERAL INFORMATION:

```

```

APPLICANT: Hillman, Jennifer L.

```

```

TITLE OF INVENTION: A NOVEL GUANOSINE MONOPHOSPHATE REDUCTASE

```

```

NUMBER OF SEQUENCES: 4

```

```

CORRESPONDENCE ADDRESS:

```

```

STREET: 3174 Porter Drive

```

```

CITY: Palo Alto

```

```

STATE: CA

```

```

COUNTRY: USA

```

```

ZIP: 94304

```

```

COMPUTER READABLE FORM:

```

```

MEDIUM TYPE: Diskette

```

```

COMPUTER: IBM Compatible

```

```

OPERATING SYSTEM: DOS

```

```

SOFTWARE: FASTSEQ for Windows Version 2.0

```

```

CURRENT APPLICATION DATA:

```

```

APPLICATION NUMBER: US/08/774.169

```

```

FILING DATE: Herewith

```

```

CLASSIFICATION: 530

```

```

PRIOR APPLICATION DATA:

```

```

APPLICATION NUMBER:

```

```

ATTORNEY/AGENT INFORMATION:

```

```

NAME: Billings, Lucy J.

```

```

REGISTRATION NUMBER: 36,749

```

```

REFERENCE/DOCKET NUMBER: PF-0182 US

```

```

TELECOMMUNICATION INFORMATION:

```

```

TELEPHONE: 415-855-0555

```

```

TELEFAX: 415-845-4166

```

```

TELEX:

```

```

INFORMATION FOR SEQ ID NO: 4:

```

```

SEQUENCE CHARACTERISTICS:

```

```

LENGTH: 345 amino acids

```

```

TYPE: amino acid

```



```

; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: PF-1612
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-625-876-2

Query Match      5.3%; Score 103; DB 1; Length 374;
Best Local Similarity 21.9%; Pred. No. 0.0095;
Matches 77; Conservative 47; Mismatches 134; Indels 94; Gaps 17;

QY 8 GGGVYPEGDLTAQOLFASADGITYNDLILPGFIDFIADVDLTSALTRKTLTKPLIS 67
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 36 GGFNTYA--GASDEWTKRANBRAMHKLLYPRLADVEAPDTSTELLHKI--KAPFTM 91
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 68 SPM-----DVTYEDAMATAMALMGIGFIHNCPPEFOANEYRKVKKFDKTLGCAAVG 121
   : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 92 APIAANGLAHTTKREATAASVEFGTMSAIVSGATFE--ELSE-----GLNG 139
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 122 TR-----EDDKYRLDLLTQAGVD-----VIVLSS--OGNS-----VYOIANVHYI 160
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 140 PRWFQIYMAKDDQNDIIDEAKSDGATAIILTDSTVSGNRDVKNFYVPEGMP--I 197
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 161 KQKY-----PHLVIGSNVYTAQAQAKNLIDAGVDGR-----VGMGC 197
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 198 VORYLRTAGSGLNINIGASKOKISPRDIEETIAHSGLPVFYKGIQHPEDADMAIKAGA 257
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 198 GSCICIOEWACGRPGGTAVYK-----VAEYARREGVPIIADGIGIOTVGHYVKAL 247
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 258 SGIWVSNH---GARQ---LYEAPGSFTLPAIAERVKN-RVPIVDSGVRGEHAKAL 309
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 248 ALGASTVMGSLAATTEAPG-----EYFSDGVRLLKRYGMSLDAME 291
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 310 ASGADVVALGRVPLFGLALGMOGAVSVLDYFQKDLTRVWQLTGSQNVEDLK 361
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 7
; US-08-625-876-4
; Sequence 4, Application US//08625876
; Patent No. 5656471
; GENERAL INFORMATION:
; APPLICANT: MINAGAWA, Hirotaka
; APPLICANT: NAKAYAMA, No. 5656471iyuki
; APPLICANT: NAKAMOTO, Shinya
; TITLE OF INVENTION: LACTATE OXIDASE WITH AN IMPROVED THERMAL
; TITLE OF INVENTION: STABILITY AND GENE OF THE SAME
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/625,876
; FILING DATE: 01-APR-1996
; CLASSIFICATION: 435

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-95947
; FILING DATE: 30-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-146186
; FILING DATE: 13-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: PF-1612
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-625-876-4

Query Match      5.1%; Score 100; DB 1; Length 374;
Best Local Similarity 22.2%; Pred. No. 0.02;
Matches 78; Conservative 48; Mismatches 132; Indels 94; Gaps 18;

QY 8 GGGVYPEGDLTAQOLFASADGITYNDLILPGFIDFIADVDLTSALTRKTLTKPLIS 67
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 36 GGFNTYA--GASDEWTKRANBRAMHKLLYPRLADVEAPDTSTELLHKI--KAPFTM 91
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 68 SPM-----DVTYEDAMATAMALMGIGFIHNCPPEFOANEYRKVKKFDKTLGCAAVG 121
   : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 92 APIAANGLAHTTKREATAASVEFGTMSAIVSGATFE--ELSE-----GLNG 139
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 122 TR-----EDDKYRLDLLTQAGVD-----VIVLSS--OGNS-----VYOIANVHYI 160
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 140 PRWFQIYMAKDDQNDIIDEAKSDGATAIILTDSTVSGNRDVKNFYVPEGMP--I 197
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 161 KQKY-----PHLVIGSNVYTAQAQAKNLIDAGVDGR-----VGMGC 197
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 198 VORYLRTAGSGLNINIGASKOKISPRDIEETIAHSGLPVFYKGIQHPEDADMAIKAGA 257
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 198 GSCICIOEWACGRPGGTAVYK-----VAEYARREGVPIIADGIGIOTVGHYVKAL 247
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 258 SGIWVSNH---GARQ---LYEAPGSFTLPAIAERVKN-RVPIVDSGVRGEHAKAL 309
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 248 ALGASTVMGSLAATTEAPG-----EYFSDGVRLLKRYGMSLDAME 291
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 310 ASGADVVALGRVPLFGLALGMOGAVSVLDYFQKDLTRVWQLTGSQNVEDLK 361
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 8
; US-08-625-876-6
; Sequence 6, Application US//08625876
; Patent No. 5656471
; GENERAL INFORMATION:
; APPLICANT: MINAGAWA, Hirotaka
; APPLICANT: NAKAYAMA, No. 5656471iyuki
; APPLICANT: NAKAMOTO, Shinya
; TITLE OF INVENTION: LACTATE OXIDASE WITH AN IMPROVED THERMAL
; TITLE OF INVENTION: STABILITY AND GENE OF THE SAME
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,876
FILING DATE: 01-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-95947
FILING DATE: 30-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-146186
FILING DATE: 13-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: PF-1612
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-625-876-6

Query Match 5.1%; Score 99; DB 1; Length 374;
Best Local Similarity 21.9%; Pred. No. 0.026;

Matches 77; Conservative 46; Mismatches 135; Indels 94; Gaps 17;

QY 8 GGTGVEDEGLTAAQULPASADGLTYNDLPLGFIPIADEVDLTSALTRKTKTLPLIS 67
DB 36 GGFNYIA--GASGDEWTKRANBRAMKHKLPRLAQDVEAPDSTELLGHKI--KAPFIM 91
QY 68 SPM-----DVTADDAIAMLAMGIGFTIHNTPEQANEVKKVKKFDKLLCGAVG 121
DB 92 APIAHSLAHTTKKAGTAAVSEGTIMISAYSATFE--EISE-----GNGG 139
QY 122 TR-----EDDKYRLDLTGAVD-----VIVLSS--QGS-----VYQIANYHI 160
DB 140 PRMGIYMAKDQNRDLDAKSDGATAILTLADSTVSGRMDVKNKFFPGMP--I 197
QY 161 KQK-----PHLYQVIGGNVYTAQAQKMLIDAGVDGLR-----VGMGC 197
DB 198 VQYRLGTAEGMSIDNIYASKOKISPRDIEIAHSGLPYFKGIQHPEDADMAIKAGA 257
QY 198 GSICITQEVMAAGRPQGTAVYK-----VAEYARREGVPIIADGGIQTGVHVKAL 247
DB 258 SGIVWSNH---GARQ---LYEADGSFDTLPLAIEVKNK--RVPIVFDGSGVGRGEHAKAL 309
QY 248 ALGASTVMGSLAATTEAPG-----EYFSDGVRLLKKYRGMGLDAME 291
DB 310 ASGADVVALGRPVLFGLALGGMGAYSLVDYFQKDLTRVMQLTGSQVVEDLK 361

RESULT 9

US-08-253-823-1

; Sequence 1, Application US/08253823

; Patent No. 5541094

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: GLYCOLATE OXIDASE PRODUCTION

; NUMBER OF SEQUENCES: 1

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM

; OPERATING SYSTEM: MICROSOFT WINDOWS V3.0

; SOFTWARE: MICROSOFT WORD V2.0C

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/253,823

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/085,488
FILING DATE: JULY 1, 1993
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-253-823-1

Query Match 4.9%; Score 95; DB 1; Length 369;
Best Local Similarity 26.6%; Pred. No. 0.069;

Matches 47; Conservative 23; Mismatches 63; Indels 44; Gaps 8;

QY 120 VGTREDD-KYR-----LDLITQAGVYVIYD---SSQGSNVYQIANYHI-----KQ 162
DB 161 LGREADIKKRFVLPPLTLTKNEGIDLGKMDXANDSSLYVAGQIDRSLSKMDVAMIQ 220
QY 163 KYPHLYQVIGGNVYTAQAQKMLIDAGVDGLRV--GMGC-----GSICITQEVMA--ACGRP 212
DB 221 TITSLPLVAGVITAEDARLAVOHGAGCITVSNHGAQOLDYVPRATIALEEVYKNAQGR- 279
QY 213 QGTAVYKVAEYARREGVPIIADGGIQTGVHVKALALGASTVMGSLAATTEAPGE 269
DB 280 -----IPVFLDGVGRGTDVFKALALGAGVFTGRPVVSLAAEGE 320

RESULT 10

US-08-290-508-3

; Sequence 3, Application US/08290508

; Patent No. 5693490

; GENERAL INFORMATION:

; APPLICANT: PAYNE, MARK S.

; APPLICANT: ANTON, DAVID L.

; APPLICANT: DICOSIMO, ROBERT

; TITLE OF INVENTION: Production of glycolate oxidase

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E. I. DU PONT DE NEMOURS

; ADDRESSEE: AND COMPANY

; STREET: 1007 MARKET STREET

; CITY: WILMINGTON

; STATE: DELAWARE

; COUNTRY: U.S.A.

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.50 INCH 1.0 MB

; COMPUTER: MACINTOSH

; OPERATING SYSTEM: MACINTOSH SYSTEM, 6.0

; SOFTWARE: MICROSOFT WORD, 4.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/290,508

; FILING DATE: 15-AUG-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/025,495

; FILING DATE: 03-MAR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: GALLEGOS, R. THOMAS

; REGISTRATION NUMBER: 32,692

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 302-892-7342

; TELEFAX: 302-892-7949

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 369 amino acids

; TYPE: amino acid

4.98; Score 95; DB 2; Length 369;

ADDRESSEE: FISH & RICHARDSON

ADDRESSEE: FISH & RICHARDSON

```
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/074,121
FILING DATE: 08-JUN-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Ventler, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 05938/043001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-5277
TELEFAX: (415) 854-0875
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-074-121-3
```

Query Match 4.88; Score 94.5; DB 1; Length 448;

Best Local Similarity 21.28; Pred. No. 0.11;

Matches 73; Conservative 41; Mismatches 120; Indels 111; Gaps 13;

```
45 IADVDLTSLTRKTLKPLISSPMQVTEADMAIAMLGIGFIHNCPTPEQANE 103
Db 44 LADFTVCIGAPSVKSYLNIPAI-----ISAETIGAVAIHPGYFLSEN-----ANF 91
QY 104 VRKVKFEDKTLGCAAVGTREDKRYRLDLTQAGVDYIVLDSQGSNSVYOIAVNHVYIKOK 163
Db 92 AEQVER-----SGFIFGPK 106
QY 164 YPHLOVIGGNVNTAAQKNLIDAGVDGLRVGMCSSICITQEVYMACRPGGTAVYKAEY 223
Db 107 AETIRLMGDKVSAIAAMK-----KAGVPC-----VPGSDGPLGDDMKNRAI 148
QY 224 ARRGVPII--ADGGIQTVG-HVYKALALGASTVMGSLAATTEARGEYFFS-DGVRLK 279
Db 149 AKRIGYVPIIKASGGGGRGRRVVRGDAELAQISIM-----TRAARAAFSNDVYME 201
QY 280 KY-----RGMG-SLDAMKSSSQKRFESEGDVKYIAQVSGSIODKGSIOK 325
Db 202 KYLENPRHVEIOVLADGGNAIYLAERDCSMQRRH-----QKVVEEAPAPGITPE 251
QY 326 FVPLYLAGIOHGGODIGARSLVLRSMYSGELKFEKRTMSAOIE 370
Db 252 LRRYIGERCACACVDIGRGAGTFEFLFENGEEFYFIEMNTRIOVE 296
```

RESULT 14
PCT-US94-06447-3

```
; Sequence 3, Application PC/US9406447
; GENERAL INFORMATION:
; APPLICANT: Calgene, Inc.
; TITLE OF INVENTION: Methods and Compositions for Modulating
; TITLE OF INVENTION: Lipid Content of Plant Tissues
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weill, Gotshal & Manges
; STREET: 2882 Sand Hill Road, Suite 280
; CITY: Menlo Park
; STATE: California
```

```
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06447
FILING DATE: 06-JUN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Ventler, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE-097/MO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 926-6200
TELEFAX: (415) 854-3713
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-06447-3
```

Query Match 4.88; Score 94.5; DB 5; Length 448;

Best Local Similarity 21.28; Pred. No. 0.11;

Matches 73; Conservative 41; Mismatches 120; Indels 111; Gaps 13;

```
45 IADVDLTSLTRKTLKPLISSPMQVTEADMAIAMLGIGFIHNCPTPEQANE 103
Db 44 LADFTVCIGAPSVKSYLNIPAI-----ISAETIGAVAIHPGYFLSEN-----ANF 91
QY 104 VRKVKFEDKTLGCAAVGTREDKRYRLDLTQAGVDYIVLDSQGSNSVYOIAVNHVYIKOK 163
Db 92 AEQVER-----SGFIFGPK 106
QY 164 YPHLOVIGGNVNTAAQKNLIDAGVDGLRVGMCSSICITQEVYMACRPGGTAVYKAEY 223
Db 107 AETIRLMGDKVSAIAAMK-----KAGVPC-----VPGSDGPLGDDMKNRAI 148
QY 224 ARRGVPII--ADGGIQTVG-HVYKALALGASTVMGSLAATTEARGEYFFS-DGVRLK 279
Db 149 AKRIGYVPIIKASGGGGRGRRVVRGDAELAQISIM-----TRAARAAFSNDVYME 201
QY 280 KY-----RGMG-SLDAMKSSSQKRFESEGDVKYIAQVSGSIODKGSIOK 325
Db 202 KYLENPRHVEIOVLADGGNAIYLAERDCSMQRRH-----QKVVEEAPAPGITPE 251
QY 326 FVPLYLAGIOHGGODIGARSLVLRSMYSGELKFEKRTMSAOIE 370
Db 252 LRRYIGERCACACVDIGRGAGTFEFLFENGEEFYFIEMNTRIOVE 296
```

RESULT 15

US-08-591-079-8

; Sequence 8, Application US/08591079

; Patent No. 5972899

; GENERAL INFORMATION:

; APPLICANT: Zychlinsky, Arturo

; APPLICANT: Chen, Yajing

; TITLE OF INVENTION: Apoptosis Induced by Shigella Ipab

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 2000 Pennsylvania Avenue, NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20006-1812

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591.079
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Livnat, Shmuel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 15661-20017.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0764
TELEX: 90-4030 MRSNFOERSM
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-591-079-8
```

```
Query Match          4.8%; Score 93.5; DB 2; Length 593;
Best Local Similarity 19.6%; Pred. No. 0.21;
Matches 72; Conservative 57; Mismatches 124; Indels 115; Gaps 17;
```

```
QY 47 DEVDLTSLTRITLTKPLISSPMDVTVEADMAIAMLGIGIFIHNTPEFOANEVRK 106
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 248 DNLNVARLTMLMAMFETLVGNKTESLQNDLALFNALDEGQAEMEKKSAEFO-BETRK 306
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 107 VKRFDKTLIC-GAAGTREDDKYRDLTLT-----QAGVDYIYLD--- 144
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 307 ABEETNNIMCICKIKYLGA-----LRTIVSVAAVFTGASLAAVGLAVMADEIV 357
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 145 -SSQGNSTYQIA---MWHYIKOKYPHLOYIGGNVYTAQAOKNLIDAGVD-----GLR 192
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 358 KAATGVSFTIOALNPLMEHYLK---PLMELIG-----KAITRALDEGLVDKKTAEWAGSI 409
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 193 VGMGCGSICITQEVN-----ACGRPGGTAVYK---VAEYARFQVPIIA 233
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 410 VCAIYVAIAIMAVIYVAVVVGKAAGAAKLNALSKMMGETIKKLVPNVLKOLAONGSKLFT 469
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 234 DG-----GIOT-----VGHVVKALALG-----ASTVMGSLIA 261
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 470 QGMQRTISGLGNVSKMGLOTNALSKELVGNLTKVALLGMEVYNTAQAAGVABGVFIK 529
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 262 ATTEAPGEYFFSDGVRLKKYRGKSLDAMEKSSSSQKRYFESGDKY--KIAQGVSGSID 319
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 530 NASEALADFM-----LAEF-----AMDQIOQWLKQSEVETIGENOKVTAELOKMASSAVQO 579
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 320 KGSIOKEV 327
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 580 NADASRFI 587
```

```
RESULT 16
US-08-591-079-10
; Sequence 10, Application US/08591079
; Patent No. 5972899
; GENERAL INFORMATION:
; APPLICANT: Zychlinsky, Arturo
; APPLICANT: Chen, Yajing
; TITLE OF INVENTION: Apoptosis Induced by Shigella Ipab
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
```

```
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591.079
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Livnat, Shmuel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 15661-20017.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0764
TELEX: 90-4030 MRSNFOERSM
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-591-079-10
```

```
Query Match          4.8%; Score 93.5; DB 2; Length 593;
Best Local Similarity 19.6%; Pred. No. 0.21;
Matches 72; Conservative 57; Mismatches 124; Indels 115; Gaps 17;
```

```
QY 47 DEVDLTSLTRITLTKPLISSPMDVTVEADMAIAMLGIGIFIHNTPEFOANEVRK 106
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 248 DNLNVARLTMLMAMFETLVGNKTESLQNDLALFNALDEGQAEMEKKSAEFO-BETRK 306
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 107 VKRFDKTLIC-GAAGTREDDKYRDLTLT-----QAGVDYIYLD--- 144
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 307 ABEETNNIMCICKIKYLGA-----LRTIVSVAAVFTGASLAAVGLAVMADEIV 357
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 145 -SSQGNSTYQIA---MWHYIKOKYPHLOYIGGNVYTAQAOKNLIDAGVD-----GLR 192
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 358 KAATGVSFTIOALNPLMEHYLK---PLMELIG-----KAITRALDEGLVDKKTAEWAGSI 409
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 193 VGMGCGSICITQEVN-----ACGRPGGTAVYK---VAEYARFQVPIIA 233
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 410 VCAIYVAIAIMAVIYVAVVVGKAAGAAKLNALSKMMGETIKKLVPNVLKOLAONGSKLFT 469
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 234 DG-----GIOT-----VGHVVKALALG-----ASTVMGSLIA 261
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 470 QGMQRTISGLGNVSKMGLOTNALSKELVGNLTKVALLGMEVYNTAQAAGVABGVFIK 529
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 262 ATTEAPGEYFFSDGVRLKKYRGKSLDAMEKSSSSQKRYFESGDKY--KIAQGVSGSID 319
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 530 NASEALADFM-----LAEF-----AMDQIOQWLKQSEVETIGENOKVTAELOKMASSAVQO 579
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 320 KGSIOKEV 327
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 580 NADASRFI 587
```

```
RESULT 17
US-08-403-866-10
; Sequence 10, Application US/08403866
; Patent No. 5643779
; GENERAL INFORMATION:
; APPLICANT: Ehrlich, Stanislaw
; APPLICANT: Godon, Jean-Jacques
; APPLICANT: Renault, Pierre
; TITLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate
; TITLE OF INVENTION: synthase from Lactococcus and its applications
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
```

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,866
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30, 727
REFERENCE/DOCKET NUMBER: 20747/30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1600
TELEFAX: (716) 263-1487
TELEX: 978450 (WUT)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Lactococcus lactis subsp. lactis
INDIVIDUAL ISOLATE: ILVA
US-08-403-866-10

```

Query Match 4.7%; Score 91.5; DB 1; Length 441;

Best Local Similarity 20.3%; Pred. No. 0.22; Matches 80; Conservative 70; Mismatches 139; Indels 105; Gaps 19;

```

QY 46 ADEVDLSALRLKTLTKPLISSP-----MDFTVTEADMAIAMLGIGFIH 93
DB 4 AKEVEDAYDLKAVYTPQLDPLYSNKYQANIYKEVTKTPQLDPL----- 54
QY 94 NCTPEFOAN-----EVRKVKF-----DKTLGCAAVGTREDDKYRL 130
DB 55 --SNKYQANIYKLEENQKVSFELRGAYYSISKLSDEORSKGVACASAGNHAGVAFMA 112
QY 131 DLTL-QAGVQIVYLDSSQGSVYQIAVHIKQYPHLOYIGGVNVAADA----- 180
DB 113 NQLIISATITPVTTPNQ-----KISQVKFFGESHVIRILGTFDESARAAAFSDOND 167
QY 181 KNLDIAGVDGLRVGCGSICITQEVNACGRPGSTAVYKVAEYARRRGVPIADGIGIOTV 240
DB 168 KPLIDP-FDDENVIAAGGVAL--EIRNAOKKQISIDKI--FVQIGGGGLIA--GITAY 220
QY 241 G-----HVKALALGASTVMMGSLIAATTAPEGEYF--FSDGVRLLKRYRGMSLDAME 291
DB 221 SKERYPOTEIIGVEAKGATS--MKAAVSACQPVYLEHIDKFAAGIAV----- 265
QY 292 KSSSSOKRYSESGDKYKVIAGVSSSIDKSIQKFPYLLAGIQHOGDIGARSLVLR 351
DB 266 -ATVGQYTLQILNKVQILAV-----DEGLISQTLIELYSKILGIYAEPAGATSVALE- 318
QY 352 MMYSGELKFEKRTMSAQIEGG---VHGLHSYERK 382
DB 319 -LIKDEIK--GKNIVCIISGNDISMQIEER 349

```

```

RESULT 18
US-09-255-502-7
; Sequence 7, Application US/09255502
; Patent No. 6218165
; GENERAL INFORMATION:
; APPLICANT: Estell, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: Mutant Proteins Having Lower Allergenic Responses in
; TITLE OF INVENTION: Humans and Methods for Constructing, Identifying and
; TITLE OF INVENTION: Producing Such Proteins
; FILE REFERENCE: GC 527-D2

```

```

CURRENT APPLICATION NUMBER: US/09/255,502
CURRENT FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: 09/060,872
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 1052
TYPE: PRT
ORGANISM: Homo sapiens
US-09-255-502-7

```

Query Match 4.7%; Score 91; DB 4; Length 1052;

Best Local Similarity 21.4%; Pred. No. 1; Matches 60; Conservative 36; Mismatches 100; Indels 84; Gaps 12;

```

QY 85 MGIGIFIHNCIP---EFOANEYRKVKKFKPTLLCGAANGTREDKXRLDLTQAGVDV- 140
DB 308 IGGPDFMDHPFDVKWELTANNVIMVSAIGND---GPLYGTLLNPPADQMDVIGVGIDFE 364
QY 141 --IVLDSQGSNYYQIAMVHIKQYPHLOYIGG-----NVTAAQAKNLIDAGVDGLR 192
DB 365 DNIAFRSSKMTTWELP-----GCGRMKPDIVT-----YAGVYRGS 402
QY 193 VGMCGSICITQEVNACGRPGSTAVYKVAEYARRRGVPIADGIGIOTGVHVKALALGAS 252
DB 403 VKGCGRL-----SGTSV-----ASPVA--GAVTLVLTSTVQKRELVP 439
QY 253 TVMGSILAAATTAPEGEYFFSDG-VRLKRYRGMSLDAMEKSS----- 295
DB 440 ASKKQALIASARRLPGVNMEEQHGKIDLRAYQIINSYKPPQASLSPSYIDLTCPCYMP 499
QY 296 --SOKRYFS-----EGDKVRIAGVSGSIDKSIQKFPV 328
DB 500 YCSOPITYGMPYVNVVTILNGMGVTGRIVDKPDMQPIPL 539

```

```

RESULT 19
US-09-268-347-49
; Sequence 49, Application US/09268347
; Patent No. 6335182
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
; FILE REFERENCE: 1038-860
; CURRENT APPLICATION NUMBER: US/09/268,347
; CURRENT FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 2314
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-268-347-49

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Query Match 4.6%; Score 90; DB 4; Length 2314;

Best Local Similarity 22.0%; Pred. No. 4.5; Matches 67; Conservative 43; Mismatches 121; Indels 74; Gaps 16;

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QY 75 EADMAIAMLGIGIFIHNCIPPEFOANEYRKVKKFKPTLLCGAANGTREDKXRL- 130
DB 89 EASIAL-----GSLAKAHN-----QALIGSKPPRRQANQKAGSHAKKESIALIG 138
QY 131 DLITQA-----GVDYIVLDSQGSNYYQIAMVHIKQYPHLOYI-----GGNVV--TAA 178
DB 139 DYLAEGDASIALIGSDLYLDRNSTNSKYPNGILSTLIQHNTVLRQIRDSNGSOKYRTAA 198
QY 179 QAKNLIDAGVDGLRVGCGSICITQEVNACGRPGSTAVYKVAEYARRRGVPIADGIGI 238
DB 199 E-----GHASTAV-----GAMAYAKGHFANAFGTSTAGNYS 231

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QY 239 -TVGHVNA-----LALG--ASTVMGSL-LAATPEAPEYFSDGVRLLKRYGMGLDA 289
      || || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 232 LAVGLTAKAEKGYTAIGSNAQAINVGAALADPFVLDY-----GIAL-----GYGSQIL 283
QY 290 MKSSSSQKRYSEGD--KVKTAGVSGSIQKSGIQKVPVLLIAGIQHCODIGARSL 347
      : : : : | | | | | | | | | | | | | | | | | | | | | |
Db 284 NNNNNNNNAVYPEGNSIKSSKATGNGLFSGS--STIKRKIIIVGAGYEDTDAVNVA 341

QY 348 VLRS 352
      | : :
Db 342 QLKAV 346

RESULT 20
US-08-453-472-5
; Sequence 5, Application US/08453472
; Patent No. 562846
; GENERAL INFORMATION:
; APPLICANT: DEAN, JURRIEN
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; TITLE OF INVENTION: BASED ON ALLOIMMUNIZATION WITH ZONA PELLUCIDA
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,472
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/038,948
; FILING DATE: 26-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,462
; FILING DATE: 20-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/364,379
; FILING DATE: 12-JUN-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4032 US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 751-6849
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLER:

```

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; FEATURE:
; NAME/KEY: ZP2
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: human ZP2 protein
US-08-453-472-5

Query Match 4.5%; Score 88; DB 1; Length 745;
Best Local Similarity 19.1%; Pred. No. 1.2; Indels 114; Gaps 18;
Matches 66; Conservative 57; Mismatches 108;

QY 93 HNCPEFOANEYRKVKKEFDKTLICGAAGSTRBDDKYRLDLTQAGVD----- 139
      | : : : | | | | | | | | | | | | | | | | | | | | | |
Db 442 HALMTDFPPSKTSRSEFMTYKCS-----RNDMLNINVESTPPVASKVGLP 492
QY 140 -VIVLDSQGSNVQ-----IANYHYIKQK-YPHLYVIGN-----VTAQAQKNLID 185
      : : | | | | | | | | | | | | | | | | | | | | | |
Db 493 FTLLIQSYPDNSYQOPYGENEYPLVRFRLROPYMEVRVLRDDPNIKVLIDCMATSTWD 552
QY 186 AG-----VDGLRVGKCGSICITQEFMAGCRPGGTAVYKVAEYARFGVPIIADGI 237
      | | | | | | | | | | | | | | | | | | | | | |
Db 553 PDSFQMNWVYDGCAYDL-----DNYQTTFHPVGSSTVTHPDH-QREDMKARA---F 600
QY 238 QTVGHVNAKALAGASTVMGSLA-----ATTEA-----PGE- 269
      : | : | : | : | : | : | : | : | : | : | : | : |
Db 601 VSEAHVLSLVYFHCSALCNRLSPDPLCSVTCPPSSSHRRATGATEAKMTVSLPGPI 660
QY 270 YFFSDGVRLLKRYGMGLDAMEKSSSQKRYSEGDVKYIAQVSGSIQKSGIQKVPV 329
      || : : | | | | | | | | | | | | | | | | | |
Db 661 LLLSD-----SFRGVGSSDLKASGSGEKRSRGTGEV-----GSRGAMDTKG-----H 706
QY 330 LIAGIHGCDIGARSLSVLRSMYSGELK-----PEKRTMS 366
      || | | : : : : : : : : : : : : : : : :
Db 707 KTAG-----DVGSKAAVAANA--FAGVATLIGFIYLYTEKRTVS 743

RESULT 21
US-08-038-948-9
; Sequence 9, Application US/08038948
; Patent No. 5641487
; GENERAL INFORMATION:
; APPLICANT: DEAN, JURRIEN
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE BASED ON
; TITLE OF INVENTION: ALLOIMMUNIZATION WITH ZONA PELLUCIDA POLYPEPTIDES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/038,948
; FILING DATE: 26-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,462
; FILING DATE: 20-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/364,379
; FILING DATE: 12-JUN-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: 99152/E-266,98/2
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-038-948-9

Query Match 4.5%; Score 88; DB 1; Length 745;
Best Local Similarity 19.1%; Pred. No. 1.2;
Matches 66; Conservative 57; Mismatches 108; Indels 114; Gaps 18;

QY 93 HNCPEQANEVRKVKFEDTLTLCGAAGVGTREDKRYRLDLTQAGVD----- 139
DB 442 HALMTDPPSKISDSEFRMTVKCSYS-----RNDMLNINVESTLPVAVSKLGP 492
QY 140 -VIVLDSQGNVYQ-----IAMVHYIKOK-YPHLOVIGN-----VYTAQAQKRLID 185
DB 493 FTLLQSYPNDSYQPPGENEYPLVRPLRQPIYMEVRLNDDPNIKLVLDCCWATSTMD 552
QY 186 AG-----VDGLRGMCGGSGICITQEVNACGRPGGTAYKVAEYARRRGVPIADGGI 237
DB 553 PDSEFQMNVVVDCAYDL-----DNYQTTFHPVGSSTVHPDHY-QREFDKMAFA--F 600
QY 238 QTVGHVVKALALAGASTVMGSLA-----ATTEA-----PGE- 269
DB 601 VSEAHVLSLVYFHCALICNRLSPDPLCSVTCPVSSRRHRATGATEAKMTVSLPGPI 660
QY 270 YFSDGVRLKKRYGMSGLDAMEKSSSQKRYFSEGDVKYIAQGVSGSIDQKSGIQKFPVY 329
DB 661 LLLSD-----SSFRGVGSSDLKAGSSGSEKSRSETEEV-----GSRGAMDTKG-----H 706
QY 330 LINGIHGCGDIGARSLSVLRSMYSGELK-----FEKRTMS 366
DB 707 KTAG-----DVGSKAVAAVA--FAGVAVATLIGFIYLYLEKRTVS 743

RESULT 22
US-08-453-952-5
Sequence 5, Application US/08453952
Patent No. 5672488
GENERAL INFORMATION:
APPLICANT: DEAN, JURRIEN
TITLE OF INVENTION: CONTRACEPTIVE VACCINE
TITLE OF INVENTION: BASED ON ALLOIMMUNIZATION WITH ZONA PELLUCIDA
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,952
FILING DATE: 30-May-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/038,948
FILING DATE: 26-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,462

FILING DATE: 20-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/364,379
FILING DATE: 12-JUN-1989
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AOTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4032 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 745
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
CELL TYPE:
TISSUE TYPE:
CELL LINE:
ORGANELLE:
FEATURE:
NAME/KEY: 2P2
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: human 2P2 protein
US-08-453-952-5

Query Match 4.5%; Score 88; DB 1; Length 745;
Best Local Similarity 19.1%; Pred. No. 1.2;
Matches 66; Conservative 57; Mismatches 108; Indels 114; Gaps 18;

QY 93 HNCPEQANEVRKVKFEDTLTLCGAAGVGTREDKRYRLDLTQAGVD----- 139
DB 442 HALMTDPPSKISDSEFRMTVKCSYS-----RNDMLNINVESTLPVAVSKLGP 492
QY 140 -VIVLDSQGNVYQ-----IAMVHYIKOK-YPHLOVIGN-----VYTAQAQKRLID 185
DB 493 FTLLQSYPNDSYQPPGENEYPLVRPLRQPIYMEVRLNDDPNIKLVLDCCWATSTMD 552
QY 186 AG-----VDGLRGMCGGSGICITQEVNACGRPGGTAYKVAEYARRRGVPIADGGI 237
DB 553 PDSEFQMNVVVDCAYDL-----DNYQTTFHPVGSSTVHPDHY-QREFDKMAFA--F 600
QY 238 QTVGHVVKALALAGASTVMGSLA-----ATTEA-----PGE- 269
DB 601 VSEAHVLSLVYFHCALICNRLSPDPLCSVTCPVSSRRHRATGATEAKMTVSLPGPI 660
QY 270 YFSDGVRLKKRYGMSGLDAMEKSSSQKRYFSEGDVKYIAQGVSGSIDQKSGIQKFPVY 329
DB 661 LLLSD-----SSFRGVGSSDLKAGSSGSEKSRSETEEV-----GSRGAMDTKG-----H 706
QY 330 LINGIHGCGDIGARSLSVLRSMYSGELK-----FEKRTMS 366
DB 707 KTAG-----DVGSKAVAAVA--FAGVAVATLIGFIYLYLEKRTVS 743

RESULT 23
US-08-484-993B-43
Sequence 43, Application US/08484993B
Patent No. 5837497
GENERAL INFORMATION:
APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: Hsu, Kuang T.

[illegible]

```

Sequence 5 Application US/08862903
Patent No. 5916768

GENERAL INFORMATION:
APPLICANT: DEAN, JURRIEN
TITLE OF INVENTION: CONTRACEPTIVE VACCINE
TITLE OF INVENTION: BASED ON ALLOIMUNIZATION WITH ZONA PELLUCIDA
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,903
FILING DATE: 30-May-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/038,948
FILING DATE: 26-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,462
FILING DATE: 20-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/364,379
FILING DATE: 12-JUN-1989
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4032 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ. ID NO.: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 745
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
FEATURE:
NAME/KEY: ZP2
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: human ZP2 protein
US-08-862-903-5

Query Match 4.5%; Score 88; DB 2; Length 745;
Best Local Similarity 19.1%; Pred. No. 1.2;
Matches 66; Conservative 57; Mismatches 108; Indels 114; Gaps 18;

0y 93 HNCIPEFOANEVRYKKKDKILLGCAVGTREDDKRYRLDLTQAGVD----- 139
db 442 HALWTDPPSKISRDSEFRMTVKCSY-----RNDMLINIVESLTPPVASYKICP 492

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2002, 08:25:31 : Search time 21 Seconds
(without alignments)
1757.062 Million cell updates/sec

Title: US-09-853-918-30

Perfect score: 1955
Sequence: 1 MADYLISGNGVHPEDGLTA.....MSAQIEGTVHGLHSYERLY 384

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :
1: PIR.71.*
2: PIR1.*
3: PIR2.*
4: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1858	95.0	514	1 A35566	IMP dehydrogenase
2	1655	84.7	514	1 B31997	IMP dehydrogenase
3	1653	84.6	514	1 A31997	IMP dehydrogenase
4	1640	83.9	514	1 UT0565	IMP dehydrogenase
5	1348.5	69.0	537	1 S41064	IMP dehydrogenase
6	1271.5	65.0	537	1 S59508	IMP dehydrogenase
7	1245.5	63.7	524	1 S50890	IMP dehydrogenase
8	1238.5	63.4	523	1 S59402	IMP dehydrogenase
9	1233.5	63.1	523	1 A54997	IMP dehydrogenase
10	1094.5	56.0	512	1 A55407	IMP dehydrogenase
11	1087.5	55.6	514	1 A38668	IMP dehydrogenase
12	1076.5	55.1	524	1 T40127	IMP dehydrogenase
13	1039.5	53.2	499	1 T32709	IMP dehydrogenase
14	1016	52.0	502	1 F86298	IMP dehydrogenase
15	1007.5	51.5	503	1 JC4999	IMP dehydrogenase
16	691.5	35.4	403	1 S53477	IMP dehydrogenase
17	674	34.5	485	2 D97232	IMP dehydrogenase
18	654.5	33.5	485	1 G81308	IMP dehydrogenase
19	649	33.2	490	1 H70473	IMP dehydrogenase
20	649	33.2	509	2 JC7305	IMP dehydrogenase
21	641.5	32.8	482	2 C72264	IMP dehydrogenase
22	632	32.3	489	2 H83173	IMP dehydrogenase
23	629	32.2	485	2 B82558	IMP dehydrogenase
24	628	32.1	485	2 D83652	inositol-monophosp
25	626.5	32.0	488	2 DEBSMP	IMP dehydrogenase
26	626	32.0	487	2 F81906	IMP dehydrogenase
27	625	31.9	487	1 H81109	IMP dehydrogenase
28	624.5	31.9	488	1 S23226	IMP dehydrogenase
29	613.5	31.4	521	1 T17196	IMP dehydrogenase

30	613	31.4	488	2 C89805	inositol-monophosp
31	610.5	31.2	529	1 F70736	IMP dehydrogenase
32	606.5	31.0	500	1 F75342	IMP dehydrogenase
33	606	30.7	404	1 E70218	IMP dehydrogenase
34	600.5	30.7	488	1 DECIIP	IMP dehydrogenase
35	600.5	30.7	488	2 B91050	IMP dehydrogenase
36	600.5	30.7	488	2 G85894	IMP dehydrogenase
37	600.5	30.7	529	1 S72823	IMP dehydrogenase
38	600	30.7	489	2 C82282	IMP dehydrogenase
39	599.5	30.7	357	1 B81701	probable IMP dehyd
40	597.5	30.6	488	2 AE1419	inosine-monophosph
41	597.5	30.6	488	2 AF1794	inosine-monophosph
42	597.5	30.6	490	2 AE0820	IMP dehydrogenase
43	589.5	30.2	487	2 AC0349	IMP dehydrogenase
44	586.5	30.0	488	2 AC0349	IMP dehydrogenase
45	585.5	29.9	499	2 AC3621	IMP dehydrogenase
46	577	29.5	493	1 JC4372	inosine-5'-monopho
47	574.5	29.4	492	2 C95260	inosine-5'-monopho
48	574.5	29.4	492	2 F98125	IMP dehydrogenase
49	574	29.4	481	1 E64623	IMP dehydrogenase
50	572	29.3	481	1 H71890	IMP dehydrogenase
51	570.5	29.2	493	2 D86652	IMP dehydrogenase
52	565	28.9	487	2 H87449	inosine-5'-monopho
53	552.5	28.3	503	2 F97434	guab protein (AE27
54	523.5	26.8	484	1 B69056	IMP dehydrogenase
55	516	26.4	473	2 AB2653	inosine-5'-monopho
56	505	25.8	496	1 G64501	IMP dehydrogenase
57	504.5	25.8	157	1 S78078	IMP dehydrogenase
58	491	25.1	485	2 E75015	IMP dehydrogenase
59	490.5	25.1	486	1 E71456	IMP dehydrogenase
60	490	25.1	485	1 JC4998	IMP dehydrogenase
61	487.5	24.9	527	2 F84256	inosine monophosph
62	487.5	24.9	527	2 F84256	inosine monophosph
63	484	22.2	246	1 C72109	IMP dehydrogenase
64	484	22.2	246	2 D86512	inosine 5'-monopho
65	384.5	20.2	444	1 D72631	probable IMP dehyd
66	384.5	19.7	503	2 A58910	IMP dehydrogenase
67	375.5	19.2	502	2 AE1091	inosine monophosph
68	373.5	19.1	502	2 AD1455	inosine monophosph
69	354	18.1	347	2 F82490	GMP reductase VC40
70	348	17.8	479	1 C70664	IMP dehydrogenase
71	339	17.3	325	1 A71887	probable GMP reduct
72	335	17.1	327	2 D97326	probable GMP reduct
73	335	17.1	345	1 B32902	GMP reductase (EC
74	331.5	17.0	328	2 G98012	GMP reductase (EC
75	326.5	16.7	328	2 A05145	conserved hypotnet
76	325	16.6	326	1 C70015	probable GMP reduct
77	324	16.6	478	1 T44751	IMP dehydrogenase
78	320.5	16.4	347	2 A80416	GMP reductase (EC
79	318	16.3	347	2 D90642	GMP reductase (EC
80	318	16.3	347	2 D85493	GMP reductase (EC
81	317	16.2	347	1 H64732	GMP reductase (EC
82	312	16.0	358	1 T03917	GMP reductase (EC
83	310	15.9	329	2 A86768	GMP reductase (EC
84	296	15.1	325	2 B89909	hypothetical prote
85	295.5	15.1	347	2 AD0520	GMP reductase (EC
86	289.5	14.8	349	2 A84954	GMP reductase (EC
87	247.5	12.7	387	2 AC1813	IMP dehydrogenase
88	245.5	12.6	387	1 S75050	IMP dehydrogenase
89	188.5	9.6	375	1 G70736	IMP dehydrogenase
90	168.5	8.6	375	1 D86957	probable inosine-5-
91	168.5	8.6	375	1 S72812	L-lactate oxidase
92	157	8.0	383	2 D86781	2-oxopropene dio
93	152	7.8	274	2 E69521	conserved hypotnet
94	151	7.7	310	2 H97338	hypothetical prote
95	148.5	7.6	321	2 A87668	conserved hypotnet
96	148.5	7.6	315	2 B83676	hypothetical prote
97	140	7.2	322	2 D87619	hypothetical prote
98	138	7.1	322	2 C70700	hypothetical prote
99	136.5	7.0	309	2 AB1346	conserved hypotnet
100	136	7.0	311	2 A87444	conserved hypotnet

ALIGNMENTS

```
RESULT 1
A35566
IMP dehydrogenase (EC 1.1.1.205) I - human
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydrogenas
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 05-May-2000
C:Accession: A35566
J:Ratsmeda, Y.; Ohno, S.; Kawasaki, H.; Konno, Y.; Weber, G.; Suzuki, K.
R. Biol. Chem. 265, 5292-5295, 1990
A:Title: Two distinct cDNAs for human IMP dehydrogenase.
A:Reference number: A35566; M0ID:90203022
A:Accession: A35566
A:Molecule type: mRNA
A:Residues: 1-514 <RNA>
A:Cross-references: GB:J05272; NID:q186393
A:Note: the sequence in GenBank entry HUMIMP, release 103, (PID:q307067) has 273-Phe, 2
C:Comment: mRNA for IMP dehydrogenase I predominated in normal leukocytes, whereas that
C:Genetics:
A:Gene: GDB:IMPDH1; SWSS2608
A:Cross-references: GDB:128085; OMIM:146690
A:Map position: 7q31.3-7q32
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homolo
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosyn
F:117-168/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:184-332/Domain: CBS homology <CBS1>
F:333-476/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:331/Active site: Cys #status predicted

Query Match 95.0%; Score 1858; DB 1; Length 514;
Best Local Similarity 73.9%; Pred. No. 9, 6e-129;
Matches 380; Conservative 1; Mismatches 3; Indels 130; Gaps 1;

QY 1 MADYLISGCTGYVPEDGTLTAQOLFASADGLTYNDFLTPGFIDEVDLTSALRKIT 60
DB 1 MADYLISGCTGYVPEDGTLTAQOLFASADGLTYNDFLTPGFIDEVDLTSALRKIT 60
QY 61 LKTPLISSPMDVTYEAADMAIAMLGIGFIHNCPTPEFQANRYKVKFED----- 111
DB 61 LKTPLISSPMDVTYEAADMAIAMLGIGFIHNCPTPEFQANRYKVKFED----- 111
QY 112 ----- 111
DB 112 ----- 111
QY 121 LSPSHVGVDLLEAKMRHGFSGIPITETGTMSKLVGIVTSRDIDFLAEKDHDTLLSEVMT 180
DB 121 LSPSHVGVDLLEAKMRHGFSGIPITETGTMSKLVGIVTSRDIDFLAEKDHDTLLSEVMT 180
QY 112 ----- 111
DB 112 ----- 111
QY 181 PRIELVVAAPAGVTLKEANELLQSKKGLPTVNDCELVAIARTDLKKRNDYPLASKDS 240
DB 181 PRIELVVAAPAGVTLKEANELLQSKKGLPTVNDCELVAIARTDLKKRNDYPLASKDS 240
QY 112 -KTLGCAAVGTREDDKYRLDLTLQAGVDVIVLSSQSGNSVYOIAMVHYIKORYPHLOVY 170
DB 112 -KTLGCAAVGTREDDKYRLDLTLQAGVDVIVLSSQSGNSVYOIAMVHYIKORYPHLOVY 170
QY 241 OKOLLGCAAVGTREDDKYRLDLTLQAGVDVIVLSSQSGNSVYOIAMVHYIKORYPHLOVY 300
DB 241 OKOLLGCAAVGTREDDKYRLDLTLQAGVDVIVLSSQSGNSVYOIAMVHYIKORYPHLOVY 300
QY 171 GGNVVTAAQAQKNLIDAGVDBLRYMGCGSICITQEVYACGRPGTAVYKAEYARRFGVP 230
DB 171 GGNVVTAAQAQKNLIDAGVDBLRYMGCGSICITQEVYACGRPGTAVYKAEYARRFGVP 230
QY 301 GGNVVTAAQAQKNLIDAGVDBLRYMGCGSICITQEVYACGRPGTAVYKAEYARRFGVP 360
DB 301 GGNVVTAAQAQKNLIDAGVDBLRYMGCGSICITQEVYACGRPGTAVYKAEYARRFGVP 360
QY 231 IADGGIQTGVGHVVKALALGASTVMGSLAATTEAPGEFFSDGVRLKKYRGMGSLDM 290
DB 231 IADGGIQTGVGHVVKALALGASTVMGSLAATTEAPGEFFSDGVRLKKYRGMGSLDM 290
QY 361 IADGGIQTGVGHVVKALALGASTVMGSLAATTEAPGEFFSDGVRLKKYRGMGSLDM 420
DB 361 IADGGIQTGVGHVVKALALGASTVMGSLAATTEAPGEFFSDGVRLKKYRGMGSLDM 420
QY 291 EKSSSSOKRYFSEBQDKYKIAQGVSGSIQDKGSIQKFPYLLIAGIQHSCODIGARSLSVLR 350
DB 291 EKSSSSOKRYFSEBQDKYKIAQGVSGSIQDKGSIQKFPYLLIAGIQHSCODIGARSLSVLR 350
QY 421 EKSSSSOKRYFSEBQDKYKIAQGVSGSIQDKGSIQKFPYLLIAGIQHSCODIGARSLSVLR 480
DB 421 EKSSSSOKRYFSEBQDKYKIAQGVSGSIQDKGSIQKFPYLLIAGIQHSCODIGARSLSVLR 480
QY 351 SMYSGELKFEKRTMSAQIEGVGHLSHYEKKRLY 384
```

```
DB 481 SMYSGELKFEKRTMSAQIEGVGHLSHYEKKRLY 514

RESULT 2
B31997
IMP dehydrogenase (EC 1.1.1.205) - Chinese hamster
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydroge
C:Species: Cricetus griseus (Chinese hamster)
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 05-May-2000
C:Accession: B31997
J:Collart, F.R.; Huberman, E.
R. Biol. Chem. 263, 15769-15772, 1988
A:Title: Cloning and sequence analysis of the human and Chinese hamster inosine-5'-mo
A:Reference number: A92676; M0ID:89008491
A:Accession: B31997
A:Molecule type: mRNA
A:Residues: 1-514 <COL>
A:Cross-references: GB:J04209; NID:q191119; PIDN:AAA36993.1; PID:q304517
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecu
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal hmo
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide bio
F:30-96/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:117-168/Domain: CBS homology <CBS1>
F:184-332/Domain: CBS homology <CBS2>
F:333-476/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:331/Active site: Cys #status predicted
```

```
Query Match 84.7%; Score 1655; DB 1; Length 514;
Best Local Similarity 63.6%; Pred. No. 7, 7e-114;
Matches 327; Conservative 31; Mismatches 26; Indels 130; Gaps 1;

QY 1 MADYLISGCTGYVPEDGTLTAQOLFASADGLTYNDFLTPGFIDEVDLTSALRKIT 60
DB 1 MADYLISGCTGYVPEDGTLTAQOLFASADGLTYNDFLTPGFIDEVDLTSALRKIT 60
QY 61 LKTPLISSPMDVTYEAADMAIAMLGIGFIHNCPTPEFQANRYKVKFED----- 111
DB 61 LKTPLISSPMDVTYEAADMAIAMLGIGFIHNCPTPEFQANRYKVKFED----- 111
QY 112 ----- 111
DB 112 ----- 111
QY 121 LSPKDRVDVFEAKARHGFSGIPITDTGRMGSRVLGISSRDIDFLKEEHRFLIEIMT 180
DB 121 LSPKDRVDVFEAKARHGFSGIPITDTGRMGSRVLGISSRDIDFLKEEHRFLIEIMT 180
QY 112 ----- 111
DB 112 ----- 111
QY 181 KREDLVVAAPAGITLKEANELLQSKKGLPTVNEDELVAIARTDLKKRNDYPLASKDA 240
DB 181 KREDLVVAAPAGITLKEANELLQSKKGLPTVNEDELVAIARTDLKKRNDYPLASKDA 240
QY 112 -KTLGCAAVGTREDDKYRLDLTLQAGVDVIVLSSQSGNSVYOIAMVHYIKORYPHLOVY 170
DB 112 -KTLGCAAVGTREDDKYRLDLTLQAGVDVIVLSSQSGNSVYOIAMVHYIKORYPHLOVY 170
QY 241 KROLLGCAAGTREDKYRLDLTLQAGVDVIVLSSQSGNSVYOIAMVHYIKORYPHLOVY 300
DB 241 KROLLGCAAGTREDKYRLDLTLQAGVDVIVLSSQSGNSVYOIAMVHYIKORYPHLOVY 300
QY 171 GGNVVTAAQAQKNLIDAGVDBLRYMGCGSICITQEVYACGRPGTAVYKAEYARRFGVP 230
DB 171 GGNVVTAAQAQKNLIDAGVDBLRYMGCGSICITQEVYACGRPGTAVYKAEYARRFGVP 230
QY 301 GGNVVTAAQAQKNLIDAGVDBLRYMGCGSICITQEVYACGRPGTAVYKAEYARRFGVP 360
DB 301 GGNVVTAAQAQKNLIDAGVDBLRYMGCGSICITQEVYACGRPGTAVYKAEYARRFGVP 360
QY 231 IADGGIQTGVGHVVKALALGASTVMGSLAATTEAPGEFFSDGVRLKKYRGMGSLDM 290
DB 231 IADGGIQTGVGHVVKALALGASTVMGSLAATTEAPGEFFSDGVRLKKYRGMGSLDM 290
QY 361 VIADGGIQTGVGHVVKALALGASTVMGSLAATTEAPGEFFSDGVRLKKYRGMGSLDM 420
DB 361 VIADGGIQTGVGHVVKALALGASTVMGSLAATTEAPGEFFSDGVRLKKYRGMGSLDM 420
QY 291 EKSSSSOKRYFSEBQDKYKIAQGVSGSIQDKGSIQKFPYLLIAGIQHSCODIGARSLSVLR 350
DB 291 EKSSSSOKRYFSEBQDKYKIAQGVSGSIQDKGSIQKFPYLLIAGIQHSCODIGARSLSVLR 350
QY 421 DKHLSSONRYFSEADKIKYAGVSGAVQDKGSIHKRYVPIYLLIAGIQHSCODIGAKSLTVOR 480
DB 421 DKHLSSONRYFSEADKIKYAGVSGAVQDKGSIHKRYVPIYLLIAGIQHSCODIGAKSLTVOR 480
QY 351 SMYSGELKFEKRTMSAQIEGVGHLSHYEKKRLY 384
DB 481 AMYSGELKFEKRTMSAQIEGVGHLSHYEKKRLY 514

RESULT 3
```

Query Match 83.9%, Score 1640, DB 1, Length 514.

```
Db      121 LSPRDVADVDEAARAHFGCIPITTDGRMSRLVGISSRDIDFLKEEHDQFLEIMT 180
Oy      112 ----- 111
Db      181 KREDIVVPAGITLTKAEAEIILQSRKKGKLPVNEDEDELVIARTDCLKNRDPLASKDA 240
Oy      112 -KTLICGAAVCTREDDDKRLDLLTQAGVDVYVLDSSGNSXYQIAMHYIKQKPHLYI 170
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      241 KQQLCGAAGTCTHEDDKRLDLLAQAGVDVYVLDSSGNSITFQINMKYTIKDKPNIQVI 300
Oy      171 GGNVYTAQAQNLIDAGVGLRVGMGCGSITCTQEVNACGRPGQTAAYKTAEYARRGVP 230
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      301 GGNVYTAQAQNLIDAGVGLRVGMGCGSITCTQEVNACGRPGQTAAYKTAEYARRGVP 360
Oy      221 IADGGIOTVGHVYKALALGASTVMKSLAATTEAPGEYFFSGVRLKRTKRGMSIDAM 290
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      361 VIADGGIOTVGHVYKALALGASTVMKSLAATTEAPGEYFFSGVRLKRTKRGMSIDAM 420
Oy      291 EKSSSGKRYFSEGGKRYVIAAGVSGSIDDKSGIQKFPYLLAGIQHSCODIGAKSLTVLR 350
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      421 DKHLSSQNRKRYSEADKIVVAGVSGAAYDKKSIHKFPYLLAGIQHSCODIGAKSLTVLR 480
Oy      351 SMVYSGELKFEKRTMSAQIEGVHGLHSYERKLY 384
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      481 AMVYSGELKFEKRTSSAQIEGVHGLHSYERKLY 514

RESULT 4
JT0565
N:Alternative names: IMP:NAD+ oxidoreductase; IMPH: inosine-5'-monophosphate dehydroge
C:Species: Mus musculus (house mouse)
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 05-May-2000
C:Accession: JT0565; A34375; S42724
R:Tiedeman, A.A.; Smith, J.M.
Gene 97, 289-293, 1991
A:Title: Isolation and sequence of a cDNA encoding mouse IMP dehydrogenase.
A:Reference number: JT0565; MUID:91153661
A:Accession: JT0565
A:Molecule type: mRNA
A:Residues: 1-514 <TIE>
A:Cross-references: Gb:M33934; NID:g198393; PIDN:AAA39311.1; PID:g309413
R:Hodges, S.D.; Pung, E.; McKay, D.J.; Renaux, B.S.; Snyder, F.F.
J. Biol. Chem. 264, 18137-18141, 1989
A:Title: Increased activity, amount, and altered kinetic properties of IMP dehydrogen
A:Reference number: A34375; MUID:90036890
A:Accession: A34375
A:Molecule type: protein
A:Residues: 125-134;182-194;289-290;439-449;456-457;459-464;466;475-478 <HOD>
R:Lightfoot, T.; Snyder, F.F.
Biochim. Biophys. Acta 1217, 156-162, 1994
A:Title: Gene amplification and dual point mutations of mouse IMP dehydrogenase assoc
A:Reference number: S42724; MUID:94153991
A:Accession: S42724
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-332; 'T',334-350; 'Y',352-482; 'W',484-514 <LIG>
A:Cross-references: EMBL:M98333; NID:g425157; PIDN:AAA20181.1; PID:g425158
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecu
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase: CBS homology: IMP dehydrogenase amino-terminal homo
C:Keywords: duplication, GMP biosynthesis; NAD; oxidoreductase; purine nucleotide bio
F:30-96/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:117-168/Domain: CBS homology <CBS1>
F:184-232/Domain: CBS homology <CBS2>
F:233-476/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:331/Active site: Cys #status predicted
```


Db 13 DGTAAEELF--SODGLSFNDFIILPGFIDFSSKYNVSGQFTKMLHLPLVSSPDFTVE 71
Qy 76 ADMIAIAMLKMGIGIFHNCTPEFOANRKYVKKF----- 110
Db 72 SSMARAAALMGIGIYIHNNCTVEODARVRSVKLYRNGFIKPKSVSPDVPVSTIRNIKS 131
Qy 111 -----DKT-----LLCGAAGTREDK 110
Db 132 EKGISGLVTEGKDYKGLLGICTKIDFVKDASAPVSYMTRENNMTVERYPKLEEA 191
Qy 111 -----DKT-----LLCGAAGTREDK 127
Db 192 MDVILNRSHGYLPVLNDEDEVVCLSRDAAVARADYPNSSLDNRNHLCAATSTREADK 251
Qy 128 YRLDILLQAGVDVLYLDDSSGNSVYQIAMVHYIKOKYRPHLOVIGSNVYTAQAOKNLIDAG 187
Db 252 GRVALLSAGIDVLYLDDSSGNTLYQVSEIRWKKTYPLEVAVAGNVVTDQAKNLIDAG 311
Qy 188 VDGLRVMGCGSICITQEVMACGRPOGTAVYKVAEYARREVPILADGIGIQTGHVYKAL 247
Db 312 ADSLRIGMGSSICITQEVLMACGRPOGTATYKVAEYARREVPILADGIGIQTGHVYKAL 371
Qy 248 ALGASTVMGSLAATTEAPGEYFFSDGVRLKYYRGMGLDAMEKSSSSQKRYFSEGDYV 307
Db 372 AVGANVAVMIGSMIACTSETPEYFFKDGMRKLYRGMGLDAMEKSSSSQKRYFSENEFL 431
Qy 308 KIAQGVSSSIDQKGSIOKFPYLLAGIOHGCODIGARSLSVLSMMYSGELKFEKRTMSA 367
Db 432 QVAGVAGVAVLDKGSVLLKLAIVHKLQASADIGEVSFDALIREKVEGYVLENNRTLLTA 491
Qy 368 QIEGCVHGLHSYERKLY 384
Db 492 QSEGAVSHLHYERKLF 508

RESULT 11
A38668
IMP dehydrogenase (EC 1.1.1.205) - Leishmania donovani
N:Alternate names: IMPDH; Inosine 5'-monophosphate dehydrogenase
C:Species: Leishmania donovani
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 16-Jul-1999
C:Accession: A38668
R:Wilson, K.; Collart, F.R.; Huberman, E.; Stringer, J.R.; Ullman, B.
J. Biol. Chem. 266, 1665-1671, 1991
A:Title: Amplification and molecular cloning of the IMP dehydrogenase gene of Leishmania
A:Reference number: A38668; MUID:91107664
A:Accession: A38668
A:Molecule type: DNA
A:Residues: 1-514 <MID>
A:Cross-references: GB:M55667; NID:9159360
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F:28-94/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:179-228/Domain: CBS homology <CBS>
F:229-472/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:327/Active site: Cys #status predicted

Query Match 55.6%; Score 1087.5; DB 1; Length 514;
Best Local Similarity 43.8%; Pred No.3.5e-72;
Matches 218; Conservative 62; Mismatches 89; Indels 129; Gaps 3;

Qy 15 EDGLTAQQLFASADGLTYNDPILPGFIDFIADDEVLTSAALRKITLTKPLTSSPMDTYT 74
Db 14 KKGCAAEELF--RGDGLTYNDFIILPGFIDFGADADVISQFTKRLRLHPYVSSPMDTIT 72
Qy 75 EADMAIAMLKMGIGIFHNCTPEFOANRKYVKKF----- 110
Db 73 ENEMAKTALMGVGLVHNNCTVEROVENVKSVKAVRNGFISPKSVSPNPTISNIRIK 132

Qy 111 ----- 110
Db 133 EKGISGLVTEGNDPHKLLGICTKIDVYVKKKDPVAVMTREKMTVERAPIOLEE 192
Qy 111 -----DKT-----LLCGAAGTREDK 126
Db 193 AMDVILNRSHGYLPVLNDEDEVVCLSRDAAVARADYPHSTLDKSGRLICAAATSTRED 252
Qy 127 KYRLDILLQAGVDVLYLDDSSGNSVYQIAMVHYIKOKYRPHLOVIGSNVYTAQAOKNLIDA 186
Db 253 KRVVAAALADVVDVLYLDDSSGNTLYQVSEIRWKKSTYPLEVAVAGNVVTDQAKNLIDA 312
Qy 187 GVDGLRVMGCGSICITQEVMACGRPOGTAVYKVAEYARREVPILADGIGIQTGHVYKAL 246
Db 313 EADGIRIGMGSSICITQEVLMACGRPOGTATYKVAEYARREVPILADGIGIQTGHVYKAL 372
Qy 247 LALGASTVMGSLAATTEAPGEYFFSDGVRLKYYRGMGLDAMEKSSSSQKRYFSEGDYV 306
Db 373 LAIGANCMGLMGLSGTETPEYFFKGVRLKYYRGMGLDAMEKSSSSQKRYFSENEFL 432
Qy 307 VKIAQGVSSSIDQKGSIOKFPYLLAGIOHGCODIGARSLSVLSMMYSGELKFEKRTMS 366
Db 433 VQVAGVAGVAVLDKGSVLLKLAIVHKLQASADIGEVSFDALIREKMYAGVLENNRSP 492
Qy 367 AOIEGCVHGLHSYERKLY 384
Db 493 AOGEGVSHLHYERKLF 510

RESULT 12
T40127
IMP dehydrogenase (EC 1.1.1.205) SPBC2F12.14c - fission yeast (Schizosaccharomyces po
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydroge
C:Species: Schizosaccharomyces pombe
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 21-Jul-2000
C:Accession: T40127; T42083
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, June 1997
A:Reference number: Z21907
A:Accession: T40127
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-524 <MOW>
A:Cross-references: EMBL:T297211; PIDN:CA810161.1; GSPDB:GNO0067; SPDB:SPBC2F12.14c
A:Experimental source: strain 972b-; cosmid c2F12
R:Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A:Reference number: Z17323; MUID:98162722
A:Accession: T42083
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 62-252; 'G', 254-262, 'P', 264-293 <YOS>
A:Cross-references: EMBL:D89106; NID:91749419; PIDN:BAAL13769.1; PID:91749420
A:Experimental source: strain PR745
C:Genetics:
A:Gene: SPDB:SPBC2F12.14c
A:Map position: 2
A:Introns: 153/1
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecu
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide bio
F:37-103/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:124-237/Domain: CBS homology <CBS2>
F:187-237/Domain: CBS homology <CBS1>
F:238-486/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:337/Active site: Cys #status predicted

Query Match 55.1%; Score 1076.5; DB 1; Length 524;

Best Local Similarity 44.18%; Pred. No. 2.3e-71;
Matches 224; Conservative 58; Mismatches 91; Indels 135; Gaps 3;

```

Oy 12 YPEEDGLTAQOOLFAS--ADGLTYNDLFLPGFIDFIADEVDTLSATKRTITLKPFISSP 69
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 17 YEKKGSLISDILIRNFGGGLFNFPLPGIDFVPNNVSLERTISNITVLTKEPFMSSP 76
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Oy 70 MDVTEDAMALMALMGIGFIHNCPTPEQANEVRYKKF-- 111
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 77 MDVTEDAMALMALMGIGFIHNCPTPEQANEVRYKKFENGFIIDPVVESPQHTVGD 136
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Oy 112 ----- 111
Db 137 VLKIRKGFSGIPITENGKLGKLVGIVTSRDVOFHKTPTPVTEVMTPREELITTAEG 196
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Oy 112 -----KTLGCAAV 120
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 197 ISLERANEMLRKKKGLPYVDKDNVLALLSLTDMKNLHPPLASKTSQDKQLMVAIAI 256
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Oy 121 GTREDDKRLDLTQAGVDVYVLDSSGNSVYQIAMVHYIKOKYPHLOVIGANNVTAQA 180
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 257 GTRDDRRRLALAEAGIDAVVIDSQGNCSFOIEMIKIKTYPKIDVIGNVVTREOT 316
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Oy 181 KNLIDAGVDGLRVGMCSSICITQEVMACGRPGGTAVYKAEARREGVPIIADGIGIOTV 240
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 317 ASLIAAGADGLRVGMCSSACTQEVMACGRQATALAOVAEFASQFEGIVADGIGIONV 376
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Oy 241 GHVYKALALGASTYMMGSLAATTEAPGEYFSDVRILKKRYGSLDAME---KSSSS 296
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 377 GHMVKSLSLGATAVMMGSLAGTETSPGEYVREGORAKSVRGMSIAMMGCTGKNNAS 436
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Oy 237 OKRIVSEDDKXKIAOGVSGSIQDKSGIOKEFVYLIAGIQHCODIGARSLSLRSMYSG 356
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 437 TGRFSEDDAVAVVAGVSGVLVDKSLRFLPYLTGTQHALODIGTKSLDELHEAVDKH 496
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Oy 337 ELKPEKFTMSAOIEGGVGHLSHYEKRLY 384
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 497 EVREELNASSAIRREGDIOGFATYERKLY 524
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|

```

RESULT 13

T32709
IMP dehydrogenase (EC 1.1.1.205) T22D1.3 - *Caenorhabditis elegans*
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; Inosine-5'-monophosphate dehydrogenase
C:Species: *Caenorhabditis elegans*
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
R:Accession: T32709
R:Geisler, C.; Bradshaw, H.; Hawkins, M.
submitted to the EMBL Data Library, December 1997
A:Description: The sequence of C. elegans cosmid T22D1.
A:Reference number: 221211
A:Accession: T32709
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-499 <GBI>
A:Cross-references: EMBL:AF039052; PTDN:AA894282.1; GSPDB:GN00022; CESP:T22D1.3
A:Experimental source: strain Bristol N2; clone T22D1
C:Genetics:
A:Gene: CESP:T22D1.3
A:Map position: 4
A:Insertion: 35/2; 85/3; 159/1; 183/3; 342/1; 412/3; 493/2
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homolog
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosyn
F:120-170/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:188-238/Domain: CBS homology <CBS1>
F:239-461/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:337/Active site: Cys #status predicted

Query Match 53.2%; Score 1039.5; DB 1; Length 499;
Best Local Similarity 43.9%; Pred. No. 1.1e-68;
Matches 221; Conservative 55; Mismatches 72; Indels 155; Gaps 5;

```

Oy 16 DGLTAQOLFASASQITTYNDLFLPGFIDFIADEVDTLSATKRTITLKPFISSPMTYRE 75
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 18 DGETVHEMMAHKAGLYNDLFLPGFIDFIADEVDTLSATKRTITLKPFISSPMTYRE 77
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Oy 76 ADMAIAMLALMGIGFIHNC--TPEQANEVRYKKF-----DKT----- 113
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 78 SGMAIYVALGIGIIGHNCPKPEDQAEVLKRYKFRQGVYVMPHCLSRSTAFMDIQIK 137
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Oy 114 ----- 113
Db 138 KKYGTGAPYTEDGRVSKLIGHVTSRDFEITMDVAGOKGTPISDINVSVDQLHGHIN 197
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Oy 114 -----LLGCAAV 121
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 198 DAPLSOKLKEHRLGLPYVNDNGELCALLCSDILKARDYPMASDYSKQQLCGAAYN 257
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Oy 122 TREDDKRLDLTQAGVDVYVLDSSGNSVYQIAMVHYIKOKYPHLOVIGANNVTAQA 181
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 258 TGRSQYTVDRVYAEAGVDVYVLDSSGNSVYQIAMVHYIKOKYPHLOVIGANNVTAQA 317
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Oy 182 NLDAGVDGLRVGMCSSICITQEVMACGRPGGTAVYKAEARREGVPIIADGIGIOTV 241
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 318 LLIDOGADGLRIGMGSSICITQDVMAVGRQGTAVYKAEARREGVPIIADGIGIOTV 377
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Oy 242 HVYKALALGASTYMMGSLAATTEAPGEYFSDVRILKKRYGSLDAMEKSSSSKRYE 301
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 378 YITKALSLGASAVMMGSLAATTEAPGEYFSDVRILKKRYGSLDAMEKSSSSKRYE 416
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Oy 302 SESDKVKIAOGVSGSIQDKSGIOKEFVYLIAGIQHCODIGARSLSLRSMYSGLAKE 361
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 417 SESDQIKVAGVSATKMDKSGCHKFIPYLRQVQHMDQIGVSLDREFEKDNGIVLKE 476
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Oy 362 KRIMSADIEGGVGHLSHYEKRLY 384
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 477 RSTNAQIEGGVGHLSHYEKRLY 499
    ||:||||:| ||:||||:||||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|

```

RESULT 14

F86298
IMP dehydrogenase (EC 1.1.1.205) - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
C:Accession: F86298
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maiti, R.; Marzla
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: AB6141; MUID:21016719
A:Accession: F86298
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-502 <STO>
A:Cross-references: GB:AE005172; NID:g4966356; PTDN:RAD34687.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
C:Keywords: GMP biosynthesis; NAD; oxidoreductase

Query Match 52.0%; Score 1016; DB 2; Length 502;
Best Local Similarity 42.0%; Pred. No. 6e-67;
Matches 210; Conservative 61; Mismatches 97; Indels 132; Gaps 2;
Oy 15 EDGLTAQOLFASADGLTYNDLFLPGFIDFIADEVDTLSATKRTITLKPFISSPMTYVT 74

[illegible]

D6	65	ESHMAAAMASLGGIGIVAHYNGCIAAQSIIROAKSLKHPIASDAQVKEPPEYITSLDAFG	124
D6	101	-----	100
D6	125	PSSFVFEVQGTMTTPKLLGIVTYSQMKRMVYEDREBKIIDYMKSCDSSDYCYPWELDFE	184
D6	101	-----	100
D6	185	KLEFLLEDKQKGFVULBERDEFTVWVVRKDDIQRVKGVPRKSPGTVGPDGEMMGAAIGTR	244
D6	101	-----ANEVRYKKKEDKT-----LLCGAAVTR	123
D6	124	EBDDTRDILLQAGYDVIVLDDSGNSVYYQIAMVHYIKQYPIHLOVIGNVVTPAAQAKNL	183
D6	245	ESDKRELEHLNVAGVNAVVLDDSGNSIYOLEMIKYKKYTPPELDVITGCVVVTMYQAQNL	304
D6	184	IDAGVGLRVMGCGSTCIQEWMAACGRPOTAUYKKAELARRGVYIINDGIGIQTGVHY	243
D6	305	IQAGVGLRVMGSGSITQTEYCAVNGGQATYAYKCSIAQSGIRPVADGSI NSGHT	364
D6	244	VKALLGASTVMGSSILATTEARGEYFFSPGVLYKKYRGMGSLDAEKRSSSQKRYFSE	303
D6	365	VKALVIGASTVMGSLFAGSTFEARGGYEYTPGRIKRIKGRMGSLSEATPK--GSDQRLCD	422
D6	304	GDKVRIAGVSGSIQDKSGIQRVYPTIAGIQHSCODIGARSLSVLYRSAMYSGELFIEKR	363
D6	423	QTKRIAGVGVAVADKGSVLYKLIRPTMNAHVAKQGFQDLASSIQSANGILRSNILRLEAR	482
D6	364	TMSAQIEGGVGHLSYEKRLY	384
D6	483	TGAADVEGVGHLSYEKSP	503

RESULT 16
S53477 IMP dehydrogenase (EC 1.1.1.205) FUN63 - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH); protein VAR073W
C:Species: *Saccharomyces cerevisiae*
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C:Accession: S53477
R:Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; Ka
submitted to the EMBL Data Library, February 1994
A:Description: Sequencing of chromosome I of *Saccharomyces cerevisiae*: analysis of th
A:Reference number: S53458
A:Accession: S53477
A:Molecule type: DNA
A:Residues: 1-403 <BUS>
A:Cross-references: EMBL:L28920; NID:q1616966; PIDN:AAC09509.1; PID:q456156; GSPDB:GMN
C:Genetics:
A:Gene: FUN63; MIPS:VAR073W
A:Map position: 1R
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecu
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
C:Keywords: GMP biosynthesis; NAD: oxidoreductase; purine nucleotide biosynthesis
F:37-103/Domain: IMP dehydrogenase amino-terminal homology <IDHC>
F:187-235/Domain: CBS homology <CBS>
F:236-403/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:335/Active site: Cys #status predicted

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F:332/Active site: Cys #status predicted
Query Match          51.5%; Score 1007.5; DB 1; Length 503;
Best Local Similarity 42.1%; Pred. No. 2.5e+66;
Matches 211; Conservative 62; Mismatches 95; Indels 133; Gaps 4;

QY  15 EDGLTAQQLFASADSLTNDPLFPGFTDLADEVDLSATLRKITLTKPLPSSMDTVT 74
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB   5  EDGFPADSLFACGYSYTTDDVLTFLPHFTSTDAVSLSRKRVPLIPCCSSPMDTVS 64
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY  75 EADMAIAMAALMGIGLFIHNHC-----TPRFQ----- 100
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

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	Query Match	35.4%;	Score 691.5;	DB 1;	Length 403;
	Best Local Similarity	41.2%;	Pred. No. 3e-43;		
	Matches 145;	Conservative 35;	Mismatches 43;	Indels 129;	Gaps
QY	16 DGLTMOQLFAS--ADGLTYNDFLIIRPTIDPIADEVDLTSALTKRIKTLKPPLISSPMDTV	73			
	: : :	:	: : :	:	
Db	21 DLSVDELMSDKIRGLAYNFLLIPGVLDASSSEVSLOTLRITNLINLPVSSPMDTV	80			
QY	74 TEADMAIMAMLMGIGTFHHHCTPEQANERYKKRPD-----	111			
	: :	:	:	:	:
Db	81 TSESNATFMALLDGIFGIHHHCTPDQAQDMVRKYKNENGFINNPIVISPTTTGEAKSM	140			

IMP dehydrogenase (EC 1.1.1.205) - Aquifex aeolicus
 C:Species: Aquifex aeolicus
 C:Date: 04-Jun-1999 #sequence-revision 04-Jun-1999 #text-change 16-Jul-1999
 C:Accession: H70473
 R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy-
 V.,
 Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A:Reference number: A70300; MUID:9819666
 A:Accession: H70473
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-490 <AOF>
 A:Cross-references: GB:AE000768; MIM:q2984249; PIND:AAOC07779.1; PID:q2984252; GB:AE00065
 A:Experimental source: Strain VFS
 C:Genetics:
 A:Gene: guaB
 C:Function:
 A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of
 A:Pathway: purine nucleotide biosynthesis
 C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homolog
 C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosyn
 F:12-78/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
 F:99-147/Domain: CBS homology <CBS1>
 F:162-210/Domain: CBS homology <CBS2>
 F:211-453/Domain: IMP dehydrogenase catalytic homology <IDHC>
 F:309/Active site: Cys #status predicted

Query Match	33.2%	Score 649;	DB 1;	Length 490;
Best Local Similarity	33.2%;	Pred. NO. 5.1e-40;		
Matches 157;	Conservative 62;	Mismatches 122;	Indels 132;	Gaps 3;

[illegible]

```

RESULT 20
JC7305
IMP dehydrogenase (EC 1.1.1.205) - Bacillus cereus
C:Species: Bacillus cereus
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 24-Oct-2000
C:Accession: JC7305; PC7086
R:Kim, S.I.; Miyamoto, T.; Honjo, K.; Iio, M.; Hatano, S.

```

Biosci. Biotechnol. Biochem. 64, 1210-1216, 2000
A:Title: Molecular cloning, overproduction and characterization of the *Bacillus cereus*
A:Reference number: JC7305
A:Accession: JC7305
A:Molecule type: DNA
A:Residues: 1-509 <K1M>
A:Cross-references: DDBJ:AB035643
A:Experimental source: strain ts-4
A:Accession: PC7088
A:Molecule type: protein
A:Residues: 1-7 <K12>
C:Genetics:
A:Gene: *impdh*
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
C:Keywords: DNA binding; GMP biosynthesis; NAD; oxidoreductase; sporulation
F:308/Active site: Cys #status predicted

Query Match	33.2%;	Score 649;	DB 2;	Length 509;
Best Local Similarity	-35.0%;	Pred. No. 5.3e-40;		
Matches 157;	Conservative 50;	Mismatches 114;	Indels 128;	Gaps 3;

[illegible]

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Db      69  LGIHKNNISIQGAEQVNDKVKRRSGVTSDDPFLTPEHQVYDAEHLMKRYISGVPPVNN 120
      :| | | | : | | | : | | |
Qy     109  -----KFDK----- 112
      : | |

```

Db 129 IDERKLVGIIITNRDMRFITQDSIKISIDVMTKEQLITAPVGTLLLEAEKILQKRYRIEMKPL 188
Qy 113 -----TLGGAAGTREDDKTKRLDLITLTAQDV 144
||| |||||
: : : : :
||| |||||

[illegible]

DB 249 VLIARHGSHKGVLDKVAEVRKATIPSLNTIAGNVAIAETAKALIEAGENVYVVGIGPUSJC 308

QY 202 ITQEVMACGRPGTAIVYKVAEYARFRFPYITADGSIQVGHVVAKALAGASTVMAGSILA 267

DB 309 TTRVYAGGVDPITTVYTCATCAERHGIPIADTSGTYSXGMVRIAGAHVVMISGNSFEA 366

Oy 262 ATTEAPGEYFFSDGVLRLKKRYGMGLDAMEKSSSQRRYFSEGDVKIAGVSGSIDKG 320
 |::||| |::|||||||::||| ::|||::||| ::|||::|||
Dd 369 GVAESPGETEITYOGNPFQFYRFGMSGVGMEK - GSKDRYFDGNKKLPLPEIEEGVPYG 420

QY 322 SIQKVFYLLAGIOHCODIGARSLSVLR 350
: | : : : | : : | : |
Db 427 PLADYVHQYVGLRAGMGYCGAQDLEFLR 455

RESULT 21
C72264
TMP dehydrogenase (EC 1.1.1.205) - *Thermotoga maritima* (strain MSB8)

C:Species: *Thermotoga maritima*
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: C72264
C:Netlon, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garratt, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.

Nature 399, 323-329, 1999
A>Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A72200; MUID:99287316
A:Accession: C72264
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1*482 <ARN>
A:Cross-references: GB:AE001789; GB:AE000512; NID:94981904; PIDN:AD36418.1; PID:9498
A:Experimental source: strain MSB8

C:Genetics:
 A:Gene: TM1347
 C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homolog
 C:Keywords: GMP biosynthesis; NAD: oxidoreductase
 E:5-71/Domain: IMP dehydrogenase amino-terminal homolog <IDIN>
 F:154-202/Domain: CBS homology <CBS>
 F:203-444/Domain: IMP dehydrogenase catalytic homology <IDC>
 F:301/Active site: Cys #status predicted

Query Match 32.8%; Score 641.5; DB 2; Length 482;
 Best Local Similarity 32.8%; Pred. No. 1.8e-39;
 Matches 157; Conservative 61; Mismatches 123; Indels 137; Gaps 4;

Qy 28 DGLTYNDPLILPGFIDFADVDLTSLTRKTLTKPLISSPMPTVEADMAIMAMMG 87
 Db 3 EALFFDDVLVPOYSEVLPKDKYIDTRTRQIRINIPLYSAAMOTYFAALAKLARSG 62
 Qy 88 IGFHHNCTPPEQANEVRKVK----- 109
 Db 63 IGIHKNLTPEQARQYIVKKTENGILYDPIYTPDKTVEALIDMAEYKIGLPPVDE 122
 Qy 110 -----FDK----- 113
 Db 123 EGRVLGLTNDVRFREKMLSKIKDMLTPREKLYVAPDISLEAKETLHQRLEKPLV 182
 Qy 114 -----LDCAAVGTREDDKYRLDLTLQAGVDVY 142
 Db 183 SKDNKVLGLITIKDMSYIEHPNARDEKRLVGAAGVSTPELMENEREKYKAGVDVY 242
 Qy 143 LDSSQGSNVYQIAMVHYIKQYKPHLOVIGGVNTAAQAKNIDAGVDGLRVGCGSIC 202
 Db 243 IDTAHGHRRVIELEMIKADYDPLPVAGVNAATPEEGEALIKAGADAVKVGVPISIC 302
 Qy 203 TOEWACGRPGGTAVYKAEVARRRGPYIADGGIQYGVHVKALALGASTVMGSLAA 262
 Db 303 TRVAVAGVLPOLTAVMESSEVARKYDPIIADGIRISGDIYKALAGAEVVMGSIYAG 362
 Qy 263 TTEAPGEYFFSDGVRLKRYKRGMSLDAMEKSSSQKRYFSEGDYKTAQVSGSIODKGS 322
 Db 363 TEEAPGETILYQGRKRYKAYRGMGSLGAMR--SGSADRYGCGENKFPPEGIEGVAPKGT 420
 Qy 323 IQKVPVPLINGIQHCQDIGARSLSVLRSMYSSELKFEKRTMAQIEGVYHGHSE 380
 Db 421 VKDVHOLVGLRSGMGYIGARTKELO-----EKAIVFKITPAGVKESHPHD 468

RESULT 22

H83173
 IMP dehydrogenase (EC 1.1.1.205) PA3770 [similarity] - Pseudomonas aeruginosa (strain PA
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: H83173
 A:Stoover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Martener, P.; Hickey, M.J.; Bt
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337
 A:Accession: H83173
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-489 <STO>
 A:Cross-references: GB:AE004796; GB:AE004091; NID:99949939; PIDN:AA607157.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: guaB; PA3770
 C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homolog
 C:Keywords: GMP biosynthesis; NAD: oxidoreductase

Query Match 32.3%; Score 632; DB 2; Length 489;
 Best Local Similarity 33.4%; Pred. No. 8.9e-39;

Matches 159; Conservative 55; Mismatches 130; Indels 132; Gaps 4;

Qy 26 SADDLYNDPLILPGFIDFADVDLTSLTRKTLTKPLISSPMPTVEADMAIMAMMG 85
 Db 5 SQELTDDVLLIPGISEVLPKDKYIDTRTRQIRINIPLYSAAMOTYFAALAKLARSG 64
 Qy 86 GGIHFHNCPTPEQANEVRKVKFD----- 111
 Db 65 GGIHKNLTPEQARQYIVKKTENGILYDPIYTPDKTVEALIDMAEYKIGLPPVDE 124
 Qy 112 ----- 111
 Db 125 EGEELVGIYTRDRLRVKPNAGTVAAIMPRDKLYTARECTPLEEKAKLYENRIEMULV 184
 Qy 112 -----KT-----LDCAAVGTREDDKYRLDLTLQAGVDVY 141
 Db 185 VDENVYRLGLVTRDIEKATKYPLASDEQGRRLRVGAAGVTDGTERVAALVAGVDVY 244
 Qy 142 VLDSSQGSNVYQIAMVHYIKQYKPHLOVIGGVNTAAQAKNIDAGVDGLRVGCGSIC 201
 Db 245 VVDTAHGHSGVIERVAVKOTPPYDVGIGGNATATAEAAKALAEAGADAVKVGIGPSIC 304
 Qy 202 ITQEWACGRPGGTAVYKAEVARRRGPYIADGGIQYGVHVKALALGASTVMGSLAA 261
 Db 305 TRVAVAGVLPOLTAIVNAALAEVGTGVPILADGIRISGDIYKALAGAEVVMGSIYAG 364
 Qy 262 TTEAPGEYFFSDGVRLKRYKRGMSLDAMEKSSSQKRYF--SEGDYKTAQVSGSIO 318
 Db 365 GTTEAPGETILYQGRKRYKAYRGMGSLGAMSGSGSSDRFQDASAEKLYPEGIGRP 424
 Qy 319 DKSSIQKVPVPLINGIQHCQDIGARSLSVLRSMYSSELKFEKRTMAQIEGVYHGHSE 374
 Db 425 YKGLASVYHOLMGGLRAAMGYTSADIQDMFT-----QPFVRIYAGMAESHVH 475

RESULT 23

B82558
 IMP dehydrogenase (EC 1.1.1.205) XF2430 [similarity] - Xylella fastidiosa (strain 9a5
 C:Species: Xylella fastidiosa
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 03-Aug-2001
 C:Accession: B82558
 A:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A82515; MUID:20365717
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: B82558
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-485 <SIM>
 A:Cross-references: GB:AE004052; GB:AE003849; NID:9107617; PIDN:AA85229.1; GSPDB:GN
 A:Experimental source: strain 9a5c
 R:Simmons, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carr
 as-Neto, E.; Docena, C.; El-Porty, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
 J.D.; Jungueira, M.L.; Kemper, E.L.; Kitaajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
 , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sava
 M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovsky-Almeida, S.; Vettore, A.L.
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF2430
 C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
 C:Keywords: GMP biosynthesis; NAD: oxidoreductase
 F:304/Active site: Cys #status predicted

A; Experimental source: strain 168

C;Genetics:

A;Gene: quai

C;Function:

A;Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule c

A;Pathway: purine nucleotide biosynthesis

C; Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal

C;Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleosides

F:11-77/Domain: IMP dehydrogenase ami

F;98-148/Domain: CBS homology <CBS1>

F;161-209/Domain: CBS homology <CBS2>

F:210-451/Domain: IMP dehydrogenase cata

Query Match	32.08;	Score 626.5;	DB 1;	Length 488;
-------------	--------	--------------	-------	-------------

Best Local Similarity 32.6%; Pred. No. 2.3e-38;

Matches 155; Conservative 61; Mismatches 126; Indels 133; Gaps 3;

Qy 26 SADDLETYPEFIDFIDEVDLTSALTRITKPTPLISSPMDVTEADMAIAML 85

Db 7 SKEGLTFDDVLLVPAKSEVLPRDVLDSVELTKTKLNIPVISAGMDVTESAMAIAMARQ 66

QY	86	GGIGFIHNCTPEFOANEVRKVKEDK-----	112
----	----	--------------------------------	-----

Db 67 GGLGIHKMSIEQQAQVDKVKRSRGVITNPFELTPDHQVDAEHLMGKYRISGVPIV 126

QY	113	-----	112
----	-----	-------	-----

Db 127 NNEEDOKLVGIITNRDLRFISDYSMKISDVMTKEELVTASVGTTLDEAEKILQHKIEKL 186

QY 113 -----TLLCGAAVGTREDDKYRLDLLTQAGVD 139

Db 167 PLVDDQNKLGITIKDIEKVEFPNSSKDIHGRLVGAAGVGTGDTMTRVKKLVEANVD 246

140 VVLBSSQGN5VYQIAMVHYIKQKYPHLOVIGNNVTAQAQKNLTDAGVDCLRVGMCCGS 199

247 VVIDIAHGHSQVLENI VIKIREI IPELNI LAGNVAIAEATRAL LEAGADV KVGIGPS 300

200 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098

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[illegible]

Search completed: September 26, 2002, 08:27:38
Job time: 127 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 26, 2002, 08:26:01 ; Search time 28.36 Seconds
(without alignments)
2342.385 Million cell updates/sec

Title: US-09-853-918-30
Perfect score: 1955
Sequence: 1 MADYIISGTVGPEDGLTA.....MSAQIEGGVHGLHSEYKRLY 384

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SPTREMBL19:**

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	1740.5	89.0	489	4	Q96NU2	Q96nu2 homo sapien
2	1646	84.2	514	11	Q91Z11	Q91z11 mus musculus
3	1323	67.7	445	11	Q9DC16	Q9dc16 mus musculus
4	1198.5	61.3	521	3	Q9P8J2	Q9p8j2 candida alb
5	1144	58.5	529	3	Q9UVL0	Q9uvl0 pneumocysti
6	1076.5	55.1	524	3	O14344	O14344 schizosacch
7	1039.5	53.2	499	5	O9GZH3	O9gzh3 caenorhabdi
8	1016	52.0	502	10	Q9ZPA0	Q9zpa0 glycine max
9	984	50.3	501	10	Q9AY75	Q9ay75 oryza sativ
10	858.5	43.9	510	5	O96387	O96387 plasmodium
11	795	40.7	392	10	Q944T1	Q944t1 glycine max
12	674	34.5	485	16	Q97FM8	Q97fm8 clostridium
13	654.5	33.5	485	16	O9PNN3	O9pnn3 campylobact
14	649	33.2	509	2	Q9RHG9	Q9rhg9 bacillus ce
15	643.5	32.9	509	2	O9RHG1	O9rhg1 bacillus ce
16	641.5	32.8	482	16	Q9XI68	Q9xi68 thermotoga

Q9hxm5	pseudomonas	16	489	32.3	632	17
Q9par5	xylella fas	16	485	32.2	629	18
Q9kn8	bacillus ha	16	485	32.1	628	19
Q9jud0	neisseria m	16	487	32.0	626	20
Q9jb5	neisseria m	16	487	32.0	625	21
Q99w19	staphylococ	16	488	31.4	613	22
Q9rt87	deinococcus	16	500	31.0	606.5	23
Q9ktw3	vibrio chol	16	489	30.7	600	24
Q9pkm2	chlamydia m	16	357	30.7	599.5	25
Q926y9	listeria in	16	488	30.6	597.5	26
Q91017	streptomyce	2	501	30.0	586	27
Q9rh0	corynebacte	2	506	29.5	577.5	28
Q9rh43	streptococc	16	492	29.4	574.5	29
Q9ciy6	lactococcus	16	493	29.2	570.5	30
Q9a7v2	caulobacter	16	487	28.9	565	31
Q97814	thermoplasm	16	485	28.6	558.5	32
Q92rt5	rhizobium m	16	500	28.5	557	33
Q983f6	rhizobium l	16	500	27.8	544	34
O26245	methanother	16	484	26.8	523.5	35
O9h1k8	thermoplasm	17	485	26.4	516.5	36
O42831	saccharomyc	157	157	25.8	504.5	37
Q9hqu4	halobacteri	16	527	24.9	487.5	38
O92912	chlamydia p	16	246	22.2	434	39
O86844	streptomyce	2	523	21.0	411.5	40
Q9p3x8	schizosacch	148	148	20.2	395.5	41
Q9ybu2	aeropyrum p	16	444	20.2	394	42
O89058	mus musculu	82	82	19.2	375	43
Q92fc7	listeria in	16	502	19.1	373.5	44
Q9kmw9	vibrio chol	16	347	18.1	354	45
Q91028	streptomyce	2	483	17.9	349.5	46
Q9dcz1	mus musculu	11	345	17.8	348	47
Q9p2t1	homo sapien	4	348	17.6	345	48
Q9zkz2	helicobacte	16	325	17.3	339	49
Q99127	mus musculu	11	348	17.3	338	50
O25525	helicobacte	16	327	17.1	335	51
Q97dk4	clostridium	16	327	17.1	335	52
Q96hd6	homo sapien	4	345	17.1	335	53
Q97ag5	streptococc	16	328	16.7	326.5	54
O05269	bacillus su	16	326	16.6	325	55
Q9nj48	onchocerca	5	364	16.5	322.5	56
Q9cfl1	lactococcus	16	329	15.9	310	57
Q99q1	streptococc	16	327	15.5	303	58
Q99ud9	staphylococ	16	325	15.1	296	59
O81282	prunus pers	10	116	14.7	288	60
P78758	schizosacch	3	232	14.6	285.5	61
Q91ca5	bacillus ha	2	281	12.8	250	62
P73853	synchocyst	16	387	12.6	245.5	63
Q91016	streptomyce	2	374	11.2	218	64
Q9c958	lactococcus	16	383	8.0	157	65
O28109	archaeoglob	17	274	7.8	152	66
Q97da4	clostridium	16	310	7.7	151	67
Q9a327	caulobacter	16	321	7.6	149.5	68
Q9rhy9	corynebacte	2	376	7.6	149	69
Q9kga2	bacillus ha	16	315	7.6	148.5	70
Q9nr9	leishmania	5	63	7.4	144.5	71
Q9f8f8	carboxydoth	2	130	7.3	142	72
Q96gp9	homo sapien	4	165	7.2	141	73
Q9a453	caulobacter	16	325	7.2	140	74
P71591	mycobacteri	16	322	7.1	138	75
Q9a7z7	caulobacter	16	311	7.0	136	76
Q9rqd7	zymomonas m	2	334	6.9	134.5	77
Q914v0	pseudomonas	16	328	6.9	134	78
Q9f7p8	uncultured	2	322	6.8	133.5	79
Q929k2	listeria in	16	309	6.8	132.5	80
Q99yd4	streptococc	16	323	6.5	128	81
Q9p635	neurospora	3	379	6.5	127.5	82
Q9fbc5	streptococc	16	324	6.5	127	83
Q93k07	lactobacill	2	366	6.4	126	84
Q9a5s5	caulobacter	16	335	6.2	122	85
Q92dk3	listeria in	16	309	6.1	120	86
O32792	amycolatops	2	357	6.1	119.5	87
O29309	archaeoglob	17	511	6.1	119.5	88
Q97m06	clostridium	16	208	6.1	118.5	89

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90 118 6.0 325 16 Q9K9K6 Q9K9K6 bacillus ha
91 116.5 6.0 198 16 Q9CCG2 Q9CGC2 lactococcus
92 116.5 6.0 358 2 Q339X9 Q339X9 amycolatops
93 116.5 6.0 365 10 Q9LJH3 Q9LJH3 arabidopsis
94 115 5.9 351 16 Q9HWH9 Q9HWH9 pseudomonas
95 114.5 5.9 333 10 Q9FNG0 Q9FNG0 arabidopsis
96 113.5 5.8 233 16 Q9T095 Q9T095 streptococc
97 113.5 5.8 363 10 Q9LJH5 Q9LJH5 arabidopsis
98 112 5.7 298 16 Q9TFS7 Q9TFS7 clostridium
99 111.5 5.7 442 16 Q986I0 Q986I0 rhizobium l
100 110 5.6 323 2 Q93QE0 Q93QE0 rhizobium m

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ALIGNMENTS

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RESULT 1
Q96NU2 PRELIMINARY: PRT: 489 AA.
AC Q96NU2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CDNA FLJ30078.FIS, CLONE BGG1200533, HIGHLY SIMILAR TO
DE INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE 2 (EC 1.1.1.205).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsui K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK054640; BAB70780.1; -
SQ SEQUENCE 489 AA; 52597 MW; 47A1273662A8C39B CRC64;

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Query Match 89.0%; Score 1740.5; DB 4; Length 489;
Best Local Similarity 74.6%; Pred. No. 1.le-122;
Matches 365; Conservative 5; Mismatches 14; Indels 105; Gaps 6;

Qy 1 MADYLISGGTGYVPEDGLTAQQLFASADGLTYNDFLILPGFIDFIDEVLTALTRKIT 60
Db 1 MADYLISGGTGYVPEDGLTAQQLFASADGLTYNDFLILPGFIDFIDEVLTALTRKIT 60

Qy 61 LKTPLISSPMDTVTADMAIAMA-----HNN-----CTPEF-----QANEVRK--- 83
Db 61 LKTPLISSPMDTVTADMAIAMA-----HNN-----CTPEF-----QANEVRK--- 106

Qy 84 ----LMG--IGFI-----HNN-----CTPEF-----QANEVRK--- 106
Db 121 ETGTMGSLKLVGIVTSKRDIDFLAEKDHDTLLSEVMPRIELVVAPAGVTLKEANEILQSK 180

Qy 107 -----VKKFDKTLCCGAAAGTREDOKYRDLTLQ 135
Db 181 KGKLPVNDCELVAIIARTDLKKNRDYPLASKDSQKQLCCGAAAGTREDOKYRDLTLQ 240

Qy 136 AGVDVIVLDSOGNSVYQIAMVHYIKQYPHLQVIGGNVNTAAQAKNLIDAGVDCGLRGM 195
Db 241 AGVDVIVLDSOGNSVYQIAMVHYIKQYPHLQVIGGNVNTAAQAKNLIDAGVDCGLRGM 300

Qy 196 GCGSICITQEVNMACRPGCTAVYKVAEYARRFGVPIIADGGITQTVGHVVKALALGASTVM 255
Db 301 GCGSICITQEVNMACRPGCTAVYKVAEYARRFGVPIIADGGITQTVGHVVKALALGASTVM 360

Qy 256 MGSLLAANTEAPGEFFSDGVRLKRYGMSLDAMEKSSSSQKRYFSEGDVKVIAQGVSG 315

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Db 361 MGSLLAANTEAPGEFFSDGVRLKRYGMSLDAMEKSSSSQKRYFSEGDVKVIAQGVSG 420
Qy 316 STQDKGSTQKFPYPIIAGIQHCQDQIGARSLSVLRSMYSGELKFEKRTMSAQIEGGVHG 375
Db 421 STQDKGSTQKFPYPIIAGIQHCQDQIGARSLSVLRSMYSGELKFEKRTMSAQIEGGVHG 480
Qy 376 LHSYEKRLY 384
Db 481 LHSYEKRLY 489

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RESULT 2

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Q91Z11 PRELIMINARY: PRT: 514 AA.
AC Q91Z11;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INOSINE 5'-PHOSPHATE DEHYDROGENASE 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010314; AAH10314.1; -
SQ SEQUENCE 514 AA; 55815 MW; 17D25A5C5EBCC439 CRC64;

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Query Match 84.2%; Score 1646; DB 11; Length 514;
Best Local Similarity 63.6%; Pred. No. 1.5e-115;
Matches 327; Conservative 29; Mismatches 28; Indels 130; Gaps 1;

Qy 1 MADYLISGGTGYVPEDGLTAQQLFASADGLTYNDFLILPGFIDFIDEVLTALTRKIT 60
Db 1 MADYLISGGTGYVPEDGLTAQQLFASADGLTYNDFLILPGFIDFIDEVLTALTRKIT 60

Qy 61 LKTPLISSPMDTVTADMAIAMAALMGIGFIHNNCTPEQANEVRKVKFFD----- 111
Db 61 LKTPLISSPMDTVTADMAIAMAALMGIGFIHNNCTPEQANEVRKVKVKYEGGFTIDPVV 120

Qy 112 ----- 111
Db 121 LSPKDRVDFEAKARHGFQGIPTDTGMRGSLVGLIISRDIDFLKEEHDRFLEEIMT 180

Qy 112 ----- 111
Db 181 KREDLVAPAGVTLKEANEILQSKKGLPIVNDDELVAIIARTDLKKNRDYPLASKDA 240

Qy 112 -KTLCCGAAGTREDOKYRDLTLTAQGVDTIVLDSOGNSVYQIAMVHYIKQYPHLQV 170
Db 241 KKQLCCGAAGTREDOKYRDLTLTAQGVDTIVLDSOGNSVYQIAMVHYIKQYPHLQV 300

Qy 171 GGNVYVTAQAQAKNLIDAGVGLRVGMCGSICITQEVNMACRPGCTAVYKVAEYARRFGVP 230
Db 301 GGNVYVTAQAQAKNLIDAGVGLRVGMCGSICITQEVNMACRPGCTAVYKVAEYARRFGVP 360

Qy 231 IADGGITQTVGHVVKALALGASTVMGSLLAATTEAPGEYFFSDGVRLKRYGMSLDAM 290
Db 361 IADGGITQTVGHVVKALALGASTVMGSLLAATTEAPGEYFFSDGVRLKRYGMSLDAM 420

Qy 291 EKSSSSQKRYFSEGDVKVIAQGVSGIQDKSGIOKFPYPIIAGIQHCQDQIGARSLSVLR 350
Db 421 DRHLSQNRVYSEADKIKVAQGVSGAVODKSGIHKFPYPIIAGIQHCQDQIGARSLSVLR 480

Qy 351 SMYSGELKFEKRTMSAQIEGGVHGLHSYEKRLY 384
Db 481 AMMYSGELKFEKRTSSAQVEGVSGLHSYEKRLF 514

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Db	241	AKNLIDAGVDALRVGMSSGSI	CITQEVLCAGRPQATAVYKSEYARRR	GVPIADGGIQN	300	
Qy	240	VGHVVALALGASTVMGSLAAT	TEAPGEYFFSDGVRLLKRYGMSLDAMEK	SSSSQKR	299	
Db	301	VGHAKALGASTVMGSLAAT	TEAPGEYFFSDGIRLLKRYGMSLDAMDKHL	SSQNR	360	
Qy	300	YFSEGDKVTKAQGVSGISQDK	SGIKFVPLYIAGIQHCGDITGARSLSVL	RRMYSGELK	359	
Db	361	YFSEADKIKVAQGVSAVDKGS	IHKFVPLYIAGIQHSCQDITGAKSLTQVR	AMMYSGELK	420	
Qy	360	FEKRTMSAQIEGGVHGLSH	VEKRLY	384		
Db	421	FEKRTSAQIEGGVHGLSH	TEKRLF	445		
RESULT	4					
Q9P872		PRELIMINARY;	PRT;	521	AA.	
ID	Q9P872					
AC	Q9P872					
DT	01-OCT-2000 (TReMBLrel. 15, Created)					
DT	01-OCT-2000 (TReMBLrel. 15, Last sequence update)					
DT	01-DEC-2001 (TReMBLrel. 19, Last annotation update)					
DE	PUTATIVE INOSINE 5-MONOPHOSPHATE DEHYDROGENASE.					
GN	IMH3.					
OS	Candida albicans (Yeast).					
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;					
OC	Saccharomycetales; mitosporic Saccharomycetales; Candida.					
OX	NCBI_TaxID=5476;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=1006;					
RC	MEDLINE=20569171; PubMed=11119495;					
RA	Beckerman J., Chibana H., Turner J., Magee P.T.;					
RA	"Single-copy IMH3 allele is sufficient to confer resistance to					
RT	mycophenolic acid in Candida albicans and To mediate transformation of					
RT	Clinical Candida species."					
FT	Infect. Immun. 69:108-114(2001).					
RL	EMBL; AF249293; AAF70813.1; -.					
DR	HSSP; P12268; 1B30.					
DR	InterPro; IPR000644; CBS.					
DR	InterPro; IPR003009; FMN_enzyme.					
DR	InterPro; IPR001093; IMP_DH_GMP_RED.					
DR	Pfam; PF00571; CBS; 2.					
DR	Pfam; PF00478; IMPDH_C; 1.					
DR	Pfam; PF01574; IMPDH_N; 1.					
DR	SMART; SM00116; CBS; 2.					
DR	PROSITE; PS00487; IMP_DH_GMP_RED; 1.					
FT	VARIANT 47 47 V -> I.					
FT	VARIANT 102 102 A -> S.					
FT	VARIANT 400 400 D -> G.					
FT	SEQUENCE 521 AA; 56267 MW; 7A1CF4DF6184FE7E CRC64;					
Query Match	61.3%;	Score	1198.5;	DB 3;	Length 521;	
Best Local Similarity	48.8%;	Pred. No.	6.7e-82;			
Matches 247;	Conservative	52;	Mismatches	74;	Indels 133;	
Gaps						
Qy	12	YVPEDGHTAQQLPASAD--GLTYNDFLLPGFDIFDITADEVDLT	TSALT	TRKTLTKTLP	LISP 69	
Db	15	YPRKDTGLSVKELDSTNFGGLTYNDFLLPGLVFPSPSAVSLET	KLTK	TKITLKSP	FPVSSP 74	
Qy	70	MDVTYADMAIALMAGGICGF	IHNC	TP	EQANR	VKKVKFD----- 111
Db	75	MDVTYENMAIHALGGIGII	HNCT	TE	QAE	EMVRKVKYENGFINDPVVISPEVTYGE 134
Qy	112	-----				111
Db	135	VKKMGEVLGTSFPVTENGKVGKLY	ITS	SRDIQ	FHD	NKSPVSEVMTKDLVGGKGIS 194
Qy	112	-----				112
Db	195	LTDGNELRRSKGKLP	IPVDA	EGN	LVSL	ISRTDLOKNODYPNASKSFHSLCCGAAIGT 254


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Db 77 MDTVTEDQMALYALLGGIGVHHNCTPEQAAAMVRKVKYENGFIIDPVPVFSPOHTVGD 136
Qy 112 ----- 111
Db 137 VLKIKETKGFSGIPITENGLKRLGKLVGIVTSRDVQFHKDTNPVTEVMTPRELITTAEG 196
Qy 112 -----KTLCCGAAY 120
Db 197 ISLERANEMLRKSKKGLPVVDKDDNLVALLSLTDLAKNLHFPPLASKTSOTKQLMVAAR 256
Qy 121 GTREDDKYRLDLLTQAGVDVIVLDSOGNSVYQIAMVHYIKQKYPHQLQVIGGNVVTAAQA 180
Db 257 GTRDDRTRLALLAAGLADAVVIVDSOGNSCFQETIMKWKTKPKYKPKYKPKYKPKYKPKY 316
Qy 181 KNLIDAGVGLRVGCGSGICITQEVMACGPRPQGTAVYKVAEYARRGVPPIADGGIQT 240
Db 317 ASLIAAGADGLRVGCGSGICITQEVMACGPRPQGTAVYKVAEYARRGVPPIADGGIQT 376
Qy 241 GHVYKALAGASTVMGSLLAATTEAPGEYFFSDGVRLLKRYGMSLDAME-----KSSSS 296
Db 377 GHVYKSLSGATAVMGGSLLAGTTESGEGYVREGQRYKSYRGMSIAAMEGTCVKNKAS 436
Qy 297 QKRYFSGDKVKIAQVSGSIQDKGSIQKVPYPIAGIQHCGCQDIGARSLSVLRSMYSG 356
Db 437 TGRYFSENDVAVRQVSGVGLVVDKGLRLLPFLYLTGLQHALQDGTGKSLDELHEAVDKH 496
Qy 357 ELKFKRTMSAQIEGGVHGLHSYEKRLY 384
Db 497 EVRFELKSSAAIREGDIQGFATYEKRLY 524
RESULT 7
Q9GZH3 O9GZH3 PRELIMINARY; PRT; 499 AA.
AC O9GZH3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE T22D1.3 PROTEIN.
GN T22D1.3
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium. ";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX Waterston R.;
RA Geisel C., Bradshaw H., Hawkins M.;
RT "The sequence of C. elegans cosmid T22D1. ";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX Waterston R.;
RA EMBL; AF039052; AAF98635.1;
DR EMBL; AF039052; AAF98635.1;
DR HSSP; P12268; I830.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
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DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 499 AA; 54298 MW; E96323563FE5D275 CRC64;

Query Match 53.2%; Score 1039.5; DB 5; Length 499;
Best Local Similarity 43.9%; Pred. No. 5.7e-70;
Matches 221; Conservative 55; Mismatches 72; Indels 155; Gaps 5;

Qy 16 DGLTAQOLFASADGLTYNDFLILPGFIDFTADEVDLTSLTRKTLTKLTPLISSPMQVTE 75
Db 18 DGETVHEMMAHKAAGLTYNDFNLPFGFVNFVHDVSLTETITKDKIKAPLVSSPMQVTE 77
Qy 76 ADMAIAMLGGGICFIHNC-TPEFQANEVRYKVKF-----DRT----- 113
Db 78 SGMAIYVWALYGGICIIHGNEPKPEDQAAEVLKVRFKQGVYVMPHCLSRDSTAFDMLQIK 137
Qy 114 ----- 113
Db 138 KKYGYTGAPVTEDEGRVSGKLIGMVTSRDFDFTMDVAGQKGTPISDIMVSDQLHLGHIN 197
Qy 114 -----LLCGAAG 121
Db 198 DAPELSKKLEHRLKGLPIVNDNGELCALLCRSLDKARDYPMASTDYDSKQLLCGAAYN 257
Qy 122 TREDDKYRLDLLTQAGVDVIVLDSOGNSVYQIAMVHYIKQKYPHQLQVIGGNVVTAAQA 181
Db 258 TRGESQYTVDRVVEAGVDVLIIDSSNGSSTYQISMLRYIKEKHPHVQVIAGNVVTRAQAK 317
Qy 182 NLIDAGVDGLRVGCGSGICITQEVMACGPRPQGTAVYKVAEYARRGVPPIADGGIQT 241
Db 318 LLIDQAGADGLRVGCGSGICITQEVMAVGAQGTAVYDVARVYANQRGIPVADGGIQT 377
Qy 242 HVKALAGASTVMGSLLAATTEAPGEYFFSDGVRLLKRYGMSLDAMEKSSSSQKRYF 301
Db 378 YITKALISLASAVMGGSLLAATTEAPGEYFWGPG-----GSFN-----P 416
Qy 302 SEGDKVIAQVSGSIQDKGSIQKVPYPIAGIQHCGCQDIGARSLSVLRSMYSGELKFE 361
Db 417 SESDQIKVAGVSAATMDRSGSCHKFIPIYLRVQHGMDIGVRSRDRFREKVDNGIVKFE 476
Qy 362 KRTMSAQIEGGVHGLHSYEKRLY 384
Db 477 RRTNAQLGEGVHLSHSEKRLY 499

RESULT 8
Q9ZPAO Q9ZPAO PRELIMINARY; PRT; 502 AA.
AC Q9ZPAO;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INOSINE MONOPHOSPHATE DEHYDROGENASE.
GN IMPDH1.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC Cao Y., Schubert K.R.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010201; CAB38030.1;
DR HSSP; P12268; I830.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 502 AA; 53407 MW; 617AB87613C36AA4 CRC64;
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Query Match 52.0%; Score 1016; DB 10; Length 502;
Best Local Similarity 43.3%; Pred. No. 3.3e-68;
Matches 215; Conservative 60; Mismatches 93; Indels 128; Gaps 3;

QY 15 EDGLTAQOLFASADGLTYNDLILPGCFIDFIADEVDLTSALTRKTLTKPLISSPMDVT 74
DB 9 EDGFTAELKLTGFSYTDVIFLPHYIDFAADAVDLSTRLLRPLAVPFVSPMDTVS 68
QY 75 EADMAIAMAALMGIGIFIHNCPTPEQA----- 101
DB 69 ESAMAAASLAGIAVHNSVPAQAALTRRAKSRVPILSDPAFAAPSVAVEHDDAFG 128
QY 102 ----- 101
DB 129 ASPFLVTDGTGTVGKLLGYVARSDWTNQTDKGLRVGYDYMAPPKPAWPNADLNKINEM 188
QY 102 -----NEVRKVKFKDTL-----LCGAAVGTREDDKY 128
DB 189 ESEKSAVALERDGEVVDLVVREEVERVGRYKPLVAPATVGADGFMGAAGVTREDDKE 248
QY 129 RDLTLTAQGVVDVILVLDSSQGSNSVQIAMVHYIKQYPHLOVIGNNVTTAAQAKNLIDAGV 188
DB 249 RLEHLVKAAGLVNVLVLDSSQGSNSVQIEMVYVYKRYPELVDVIGNNVTTAAQAKNLIDAGV 308
QY 189 DGLRVGMCSSGICITQEVNMACGRPGTAVKYAEYARRFGVPIADGGITQTVGHVVKALA 248
DB 309 DGLRVGMCSSGICITQEVNMACGRPGTAVKYAEYARRFGVPIADGGITQTVGHVVKALA 368
QY 249 LGASTVMGSLLAATTEAPGEYFFSDGVRLKRYGMSLDAMEKSSSKRYFSEGDVKV 308
DB 369 LGASTVMGSLLAATTEAPGEYFFSDGVRLKRYGMSLDAMEKSSSKRYFSEGDVKV 426
QY 309 IAQVSGSIODKSGTOKFPVPIYLIAGIHCQDQIGARSLSVLRSMYSGELKFEKRTMSAQ 368
DB 427 IAQVVGAVKDGKSVLNFIPYTLQAVRQGFQDQIGASSIQSAHDLRLRLRLEVRGAAQ 486
QY 369 IEGVHGLHSYEKRLY 384
DB 487 VEGGVHGLVSEKRYF 502

RESULT 9
QYAY75 PRELIMINARY; PRT; 501 AA.
ID Q9AY75;
AC Q9AY75;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE PUTATIVE INOSINE MONOPHOSPHATE DEHYDROGENASE.
GN OSUNBA0091J19.1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
RA Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSUNBA0091J19 genomic sequence.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC084320; AAK09225.1; -;
DR HSSP; P12268; 1B30.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.

SQ SEQUENCE 501 AA; 52655 MW; DDE295CB714C3802 CRC64;
Query Match 50.3%; Score 984; DB 10; Length 501;
Best Local Similarity 41.5%; Pred. No. 8.5e-66;
Matches 205; Conservative 64; Mismatches 99; Indels 126; Gaps 3;

QY 15 EDGLTAQOLFASADGLTYNDLILPGCFIDFIADEVDLTSALTRKTLTKPLISSPMDVT 74
DB 10 DDGFPAPRLFGSGVSYTDVIFLPGYIGFPADAVDLSTRLSRRIPLSIPCVASPMDTVS 69
QY 75 EADMAIAMAALMGIGIFIHNCPTPEQA----- 101
DB 70 EAMAAAMASLAGIAVHNSVPAQAALTRRAKSRVPILSDPAFAAPSVAVEHDDAFG 129
QY 102 ----- 101
DB 130 HDYGLVTERGDSLSKLVGAVAAETSSRQAPLPVSEYMRPAPRSVSASFDFEQAAAFAD 189
QY 102 -----NEVRKVKKF-----DKTLGCAAGVTREDDKYRL 130
DB 190 EGLDYAPLVSDSEVIDLITVNDVERISYKPKLGRKPSLGADGKFVVAASIGTREDDKRL 249
QY 131 DLLTQAQGVVDVILVLDSSQGSNSVQIAMVHYIKQYPHLOVIGNNVTTAAQAKNLIDAGV 190
DB 250 EQLVKAAGANAVVLDSSQGSNSVQIDMIKYAKKMYPEVDLIGNNVTTAAQAKNLVAGVDG 309
QY 191 LRVGMGSGSICITQEVNMACGRPGTAVKYAEYARRFGVPIADGGITQTVGHVVKALA 250
DB 310 LRVGMGSGSICITQEVNMACGRPGTAVKYAEYARRFGVPIADGGITQTVGHVVKALA 369
QY 251 ASTVMGSLLAATTEAPGEYFFSDGVRLKRYGMSLDAMEKSSSKRYFSEGDVKV 310
DB 370 ASTVMGSLLAATTEAPGEYFFSDGVRLKRYGMSLDAMEKSSSKRYFSEGDVKV 427
QY 311 QGVSGSIODKSGTOKFPVPIYLIAGIHCQDQIGARSLSVLRSMYSGELKFEKRTMSAQ 370
DB 428 QGVVGAVKDGKSVLNFIPYTLQAVRQGFQDQIGASSIQSAHDLRLRLRLEVRGAAQ 487
QY 371 GGVHGLHSYEKRLY 384
DB 488 GGVHGLVSEKRYF 501

RESULT 10
O96387 PRELIMINARY; PRT; 510 AA.
ID O96387
AC O96387;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DE PUTATIVE INOSINE MONOPHOSPHATE DEHYDROGENASE.
GN OSUNBA0091J19.1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
RA Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSUNBA0091J19 genomic sequence.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC084320; AAK09225.1; -;
DR HSSP; P12268; 1B30.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 510 AA; 56148 MW; 449413AD3E41A7D0 CRC64;

Query Match 43.9%; Score 858.5; DB 5; Length 510;

Qy	152	YQTAMWYIIKQKHPIHLOVIGCNVVYTAQAKNLIDAGVDGLRVMCGSGSICITIQEWMACGR	211
Dd	161	YQEMWKYVKRVVPYELDVIIGNVVTMYQAENLIQAGVDGLRVMGMSGISCTTQTEVCVAGR	271
Qy	212	PGTFATVKVAEYARREGVPTIADGGIQTGVGHVVKALAGASTVMMGSLLAATTAAPGEYF	271
Dd	221	GOATAVTKVSSIAVKSGPVPAOGGTNSNGHIYKVALSLGSTVMMGSFLAGSLAECAFY	280
Qy	272	FSDGVRLLKKYRGMSGLSDAMEKSSSKOKRYPESEGDVKYKIAQVGSGSIQDKSGIQKFYPYLI	331
Dd	281	YQNGORVKYKRGMSLEAMTKGSDA--RYLGDTAKLKIAQGVGVAVKDGKSVLNFPYTL	338
Qy	332	AGTOHGQODTGANSLSVLRSMTYSSELKF---EKRTMSAQIEGCVHGLSHSYERLY	384
Dd	339	QAVRQGFDICANSLQSAHDLLRSRLRGPGPWSSTSWKVE--FMGLVSYERKYF	392
RESULT 12			
ID	Q97FW8	PRELIMINARY; PRT; 485 AA.	
AC	Q97FW8;		
DT	01-OCT-2001 (TrEMBLrel. 18, Created)		
DT	01-OCT-2001 (TrEMBLrel. 18, Last sequence update)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE	IMP DEHYDROGENASE.		
GN	CAC2701.		
OS	Clostridium acetobutylicum.		
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;		
OC	Clostridium.		
OX	NCBL_TaxID=1488;		
RN	[]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=ATCC 824 / DSM 792 / VKM B-1787;		
RX	MEDLINE=213593325; PubMed=11466286;		
RA	Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,		
RA	Gibson R., Lee H.M., Dubois J., Doucette-Stamm L., Soucaille P., Daly M.J.,		
RA	Tatusov R.L., Sabatche F., Koonin E.V., Smith D.R.;		
RA	Bennett G.N., Koonin E.V., Smith D.R.;		
RT	*Genome sequence and comparative analysis of the solvent-producing		
RT	bacterium Clostridium acetobutylicum.*;		
RL	J. Bacteriol. 183:4823-4838(2001).		
DR	EMLB; AE007768; AAK80647.1; .		
DR	InterPro; IPR000644; CBS.		
DR	InterPro; IPR003009; FMN_enzyme.		
DR	InterPro; IPR001093; IMP_DH_GMP_RED.		
DR	Pfam; PF00571; CBS; 2.		
DR	Pfam; PF00478; IMPDH_C; 1.		
DR	Pfam; PF01574; IMPDH_N; 1.		
DR	SMART; SM00116; CBS; 2.		
DR	PROSITE; PS00487; IMP_DH_GMP_RED; 1.		
KW	Complete proteome.		
SQ	SEQUENCE 485 AA; 52188 MW; 994DIC5347F7A367 CRC64;		
Query Match 34.5%; Score 674; DB 16; Length 485;			
Best Local Similarity 35.4%; Pred. No. 1.6e-42;			
Matches 168; Conservative 52; Mismatches 118; Indels 136; Gaps			
Qy	31	TYNDFLLIPGFIDFIADVDLTSLTRKIYLIKTPLISSPMDTVTETADMATAMALMGIGF	90
Dd	10	L::: L::: : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::	69
Qy	91	IHNCTPEFOQANEVRKVK-	108
Dd	70	IHKNTTAEQASEVDVRKRQENGVIITNPISLSDNSVQEALDLMKRYRISGVPTDNAGK	129
Qy	109	- - - - -KFDK- - - - -	112
Dd	130	LIGITNPDIVFTDYSKKIEELMTTENLYTAPQGTIDEAKNLLKKHKIEKLPLVDENF	189
Qy	113	- - - - -TLCGAAVGTREDDKYRIIDLTLTQAGDVIVLDSS	146
Dd	190	VLKGLITIKTEIKTKRPFNAKDSOGRLLCAGGVGVTKMDMRVKALVDASVDVILDTA	249

DB	130	LIGIITNRD	IVFETDYSKKIEELMTTEN	LYTAPOGTTIDEAKNLLKKHKIEKLPVDENF	1899
Qy	109	-----	-----	-----KFDK-----	1112
DB	130	LIGIITNRD	IVFETDYSKKIEELMTTEN	LYTAPOGTTIDEAKNLLKKHKIEKLPVDENF	1899
Qy	113	-----	-----	-----TLGCAAVGTREDDKRYRLDLTLQAGDVIVLDSS	1461
DB	190	VLKGLITIK	IEKTRKFPNAAKDSOGRLLC	CAAGVGTDMMDRKYKALVADSAVDVIVLDTA	2491

Oy	147	QGNVYQIAMVHYIKQYPHQLQVIGNVVVTAQAQKNLIDAGVDGLRVGMCGSICITQEV	206
Dd	250	HGHSQGVLEAVKTIKKAYPELQVIAGNAVATAAAVHDLTIEAGADCVKVGIPGSGICTRWV	309
Oy	207	MACGRPGCTATYKVAEYARRRGVPPIADGGTQTGVHVVKALAGASTVMGSLLAATTEA	266
Dd	310	AGIGVPLQIATMDCVEANKGVPIIIDAGGTGYSDGIYKALAAGA KAVMMGSMFAGCEEA	369
Oy	267	PGEYFFSDGVRLLKYRGMGSIDAMEKSSSKRYFSFGDKVIAQVSGSIQDGKSIOKF	326
Dd	370	PGETEIYGRSYKYVRMGSLAAWQ--CGSKDRIFQEGNKKLVPBGVGRVPFRGVSILET	427
Oy	327	VPLYIAGIHQCQDIGARSLSVLRSMMYSGLKEFKRTMSAQIEQGIVGHLSHYE	380
Dd	428	VFIILGIRSGMGLVSRNMTEL-----FEKATFVVQTSAGLRSHPHD	471
 RESULT 13 Q9PNN3 PRELIMINARY; PRT; 485 AA.			
ID	Q9PNN3	OP9NN3	
AC	OP9NN3	01-OCT-2000 (TREMBLrel. 15, Created)	
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205).		
GN	GUAB OR CJ1058.		
OS	Campylobacter jejuni.		
OC	Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;		
CC	Campylobacter.		
OX	NCBL_Taxid=197;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=NCTC 11168;		
EX	MEDLINE=20150912; PubMed=10698204;		
RA	Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,		
RA	Basham D.J., Chillingworth T., Davies R.M., Felkwell T., Holtroyd S.,		
RA	Quail K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,		
RA	Jagals M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,		
RA	Whitehead S., Barrall B.G.;		
RT	"The genome sequence of the food-borne pathogen Campylobacter jejuni		
RT	reveals hypervariable sequences."		
RL	Nature 403:665-668(2000).		
DR	EMBL; ALJ39077; CAB73314.1; -.		
DR	HSP; P12268; 1B30.		
DR	InterPro: IPR000644; CBS.		
DR	InterPro: IPR003009; FNN_enzyme.		
DR	InterPro: IPR001093; IMP_DH_GMP_RED.		
DR	Pfam; PF00571; CBS; 2.		
DR	Pfam; PF00478; IMPDH_C; 1.		
DR	Pfam; PF01574; IMPDH_N; 1.		
DR	SMART; SM00116; CBS; 2.		
DR	PROSITE; PS00487; IMP_DH_GMP_RED; 1.		
KW	Complete proteome.		
SQ	SEQUENCE 485 AA; 52151 MW; 634332666B963CDF CRC64;		
 Query Match 33.5%; Score 654.5; DB 16; Length 485; Best Local Similarity 34.5%; Pred. No. 4.8e-41; Matches 165; Conservative 57; Mismatches 107; Indels 149; Gaps 8;			
Oy	30	LTYNDFLPCFDIFADEVDLTSAITRKTLTKPLISSPMDDTTEADMTAMALMGIG	89
Dd	8	LTFDEVLLRPGYSEVLPKEVHIHTKLNTLNMLPLISAAMDVTETHERAIMARLGIG	67
Oy	90	FIIHNCTPEFOANEVRKYKPF-	112
Dd	68	VIHKMDIASQREVKRKKGESGVIIDPIFVSPKASVAEALMAEYRISGVPVDEDK	127
Oy	113	TLL-----	115
Dd	128	KLIGILNRDLRFESDFSNLVENYTMKPLITAPGCTLDDAEKIFSTNKKELPIVDEQ	187

Qy	116	-----CGAAVGTREDDKVRLLLTQAQVDVIVLDS	145
		: : : : : : : : :	
Db	188	GRLEGLITIKDKRRKKEYEPANKDNFGRLRVGAAGVQMD--RVDALVEAGVDVVVVLDS	245
Qy	146	SQGSNVVYQIAWVHYIKOKYPHLQVIGNVVYTAOAKNLIDAGVDGLRVGMGCGSICITQE	205
		: : : : : : : : : : : : : : : : : :	
Db	246	AHGSHKGIIDTVRAIKAKYKPNLDLIAGNIATAAAKALCEAGVDVAVKVGIGPGSICITRI	305
Qy	206	VMACGRPQGTAVYKYVAEYARRFGVPIIADGGIQTGVHVVKALGALGASTVNMGSLAATTE	265
		: : : : : : : : : : : : : : : : : :	
Db	306	VSGVGVPQISNAIDECVEANKFGVPVIADGGIKYSGDIKALAVGASSVMIGSLLACTDE	365
Qy	266	APGEYFFSDGVRLLKRYRGMGSLDAMEKSSSSQKRYFSEG---DKVKIAQGVSGSIQDKGS	322
		: : : : : : : : : : : : : : :	
Db	366	SPGELFTYQGRQYKSYRGMGSLGAMQKGSSD--RYFQOQTAQDKL-VPEGIEGRVFPVGS	422
Qy	323	IQKFPVYLIIAGIQHCQDIIAGRSLSVLRSMMYSGELKFEKRTMSAQI-----EGGVH	374
		: : : : : : : : : : : : : : :	
Db	423	IRSVYHLLGLLRSSMGVYGAKDIE-----DFQKRAEFVEITTAGLKESHVH	469
RESULT	14		
Q9RHG9			
ID	Q9RHG9	PRELIMINARY; PRT; 509 AA.	
AC	Q9RHG9		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)		
DE	IMP DEHYDROGENASE.		
GN	IMPDH.		
OS	Bacillus cereus.		
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;		
OC	Bacillus/Staphylococcus group; Bacillus.		
OX	NCBI_TaxID=1396;		
ON	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=TS-4;		
RA	Kim S., Miyamoto T., Honjoh K., Iio M., Hatano S.;		
RT	Molecular cloning, Overproduction and Characterization of the		
RT	Bacillus cereus IMP dehydrogenase.";		
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB035643; BAA88235.1; -.		
DR	HSSP; P50099; 1zFJ.		
DR	InterPro; IPR000644; CBS.		
DR	InterPro; IPR003009; FMN_enzyme.		
DR	Pfam; PF00571; CBS; 2.		
DR	Pfam; PF00478; IMPDH_C; 1.		
DR	Pfam; PF01574; IMPDH_N; 1.		
DR	SMART; SM00116; CBS; 2.		
DR	PROSITE; PS00487; IMP_DH_GMP_RED; 1.		
SQ	SEQUENCE 509 AA; 55393 MW; 9E6ACB3872C4A451 CRC64;		

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Query Match      33.2%; Score 649; DB 2; Length 509;
Best Local Similarity 35.0%; Pred. No. 1.3e-40;
Matches 157; Conservative 50; Mismatches 114; Indels 128; Gaps 3;

QY      28 DGLNYNDFLLPGLFDFTADEVDLTSALTRKTIKTLPLISSPMDTVTETADMAIAMALMGG 87
       :| | | :| | | :| | :| | :| | :| | :| | | | | | | | | | | | | |
Db      9 EGLTFDVLVPARSDILPREVSKTVLSLSQLNIPLISAGMTVTETADMAIAROGG 68

QY      88 IGFTHHNTPEFOANVRKKV----- 108
       :| | | :| | | :| | | | | | | | | | | | | | | | | | | | | |
Db      69 LGIITHKNMSIEQAQEDVKVRSSGVISDPFFLTPEHQVYDAEHLMKYRISGPVVNN 128

QY      109 -----KFDK--- 112
               :| |
Db      129 LDERKLVGITNRDMRFIDYSIKISDWTKYQLTAPVGTTLTEAEKILOKYKIEKLPL 188

QY      113 -----TLLCGAAVGTREDDKYRLDLLTQAQVDVI 141
               || | | | | :| | | | | | | | | | | | | | | | | | |
Db      189 VDNNGVLOGLTIKDIEKVIEFPNSAKDKGRLLVGAAGVYTADAYLRIDALVRASVDAI 248

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Db 183 SKDNKLVGTTIKDMSVIEHPNARDEKRLVGAAGVTSPTMBRVERKLVKAGVDVIV 242
QY 143 LSSQSGNSVYQIAMVHYIKQYPLHQLVIGGNVYTAQAQKNLIDAGVGLRVGMCGSGICI 202
Db 243 IDTAHGHRSRVETLEMIKADYDLPVAVGNATPCTEALIKAGADAVKVGPGSICT 302
QY 203 TOEVMACRPOGTAVYKVAEYARRFGVPIIADGGIQTGVHVVKALGALGASTVMGSLAA 262
Db 303 TRVAVGVGVPQLTAVMECSVARKYDVPDIADGGIRYSGDIVKALAAAGAESVNVGSIKAG 362
QY 263 TTEAPEYEFSDGVRLLKRYKRGMSLDAMEKSSQSKRYFSEGDVKYKIAQVSGSIDKGS 322
Db 363 TEAPGETILYQGRKYKAYKRGMSGLAMR--SGSADRYQOEGENKFPVPEGIEMVYKGT 420
QY 323 IOKFVPIYLIAGIQHGGODIGARSLVSRMYSGLKFEKRTMSAQIEGVHGLHSYE 380
Db 421 VKDVHQLVGLRSGMYIGARTIKELQ-----EKAVFVKITPAGVKESHPHD 468
RESULT 17
Q9HXM5 PRELIMINARY; PRT; 489 AA.
AC Q9HXM5;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE.
GN GUAB OR PA3770.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.F., Erwin A.L., Mizoguchi S.D., Warren P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.J., Gollery L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen."
RL Nature 406:959-964(2000).
DR EMBL; AE004796; AAG07157.1; -.
DR HSSP; P49058; 1EEP.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Complete proteome.
SQ SEQUENCE 489 AA; 51707 MW; 6D2320AFD52C888B CRC64;

Query Match 32.3%; Score 632; DB 16; Length 489;
Best Local Similarity 33.4%; Pred. No. 2.4e-39;
Matches 159; Conservative 55; Mismatches 130; Indels 132; Gaps 4;

QY 26 SADGLTYNDFILPGFDIFADVDLTSALTRKILTKPLISSPMDTVEADMAIAML 85
Db 5 SQEALTFDDVLLPGYSEVLPKDVLSKRLTRGIELNPLVSAAMDVTEARLAIAMAQE 64
QY 86 GGIGIHHNCTPEFOANEVRKYKFD----- 111
Db 65 GGIGIHHNMGTQQAQAEVRKYKHTAIVRDPVTVTPSTKIQLLOMAREYGFSGFPV 124
QY 112 ----- 111

Db 125 EOGELVGIWTRDLRVKPNAGDTVAAMTPKDKLVTAAREGTPLEEMKAKLYENRIEKLIV 184
QY 112 -----KT-----LIGAAVGTREDDDKYRLDLLTQAGVDVI 141
Db 185 VDENVYLRGLVTRDIEKAKTYPLASKDQGRRLRVGAAGVGTGADTGERVAALVAGVDV 244
QY 142 VLDSQSGNSVYQIAMVHYIKQYPLHQLVIGGNVYTAQAQKNLIDAGVGLRVGMCGSGIC 201
Db 245 VVDTAHHGSKGVIERVVRVKQTFPDVQVIGGNIATAEAAKALAEAGADAVKVGIPGSGIC 304
QY 202 ITQEVWACRPOGTAVYKVAEYARRFGVPIIADGGIQTGVHVVKALGALGASTVMGSLLA 261
Db 305 TTRIVAGVGVPOISAIYANVAALAECTGVPLIADGGIRFSGDLAKAMVAGAYCVMGSMFA 364
QY 262 ATTEAPGEVFEFSDGVRLLKRYKRGMSLDAMEKSSQSKRYF---SEGDKVKIAQVSGSIQ 318
Db 365 GTEAPGEIETLFOGRYSYKRGMSGLGAMSGSGSDRYFQDASAGAELVPEGIEGRVP 424
QY 319 DKSGIQKFPYLIAGIQHGGODIGARSLVSRMYSGLKFEKRTMSAQIEGVH 374
Db 425 YKGALSATVHQLMGLRAAMGYTGSADIQOMRT-----QPQFVRITGAGMAESHVH 475
RESULT 18
Q9PAR5 PRELIMINARY; PRT; 485 AA.
AC Q9PAR5;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE.
GN XF2430.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
Ho P.L., Hohelsel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshuko M.H.,
Vallada H., Van Sluys M.A., Verjovsky-Almeida S., Vettore A.L.,
Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa";
RL Nature 406:151-159(2000).
DR EMBL; AE004052; AAF85229.1; -.
DR HSSP; P49058; 1EEP.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.

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DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KW Complete proteome.
SQ SEQUENCE 485 AA; 52188 MW; 8D20307B24FAAB90 CRC64;

Query Match 32.2%; Score 629; DB 16; Length 485;
Best Local Similarity 33.3%; Pred. No. 4e-39;
Matches 158; Conservative 61; Mismatches 121; Indels 134; Gaps 5;

QY 27 ADGLTYNDFLLPFGIDFIDAEVDLTSAITRKITLKTPLISSPMDVTVEADMAIAMAALMG 86
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 AEALTYDDVSLVPSHVSFVLPKDVNLETRLNIRLKLPLVLSAAMDVTVEARLAIVMAQLG 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 87 GIGFIHNCTPEFOANEVRKVKFDK----- 112
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 66 GIGIHKNLTIQOQVAEVTVKVYESGVIIRDPIITVPETSIIRDVLALTRAKNISGVPPVD 125
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 113 ----- 112
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 126 KGQLIGLVTHRDMRFESELDPPVHRHMTKKEALVTYVKEGADSQEVLLQHLHKHRIEKLTV 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 113 ----- 112
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 186 NDAPELRGLITVKDIQKSDYPNAKDAVTRLLVGAAGVGGETERRVETLAAAGVDVII 245
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 143 LSSQSGNSVYQIAMVHIKQYKPHLVIGGNVYTAQAQKLNIDAGVDGLRVGMCGSGICIT 202
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 246 VDTAHGYSGQVLDRAVAMIKRYFPOLQYIGGNVITGDAALMDAGADAVKVGVPGSICT 305
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 203 TOEYMACGRPQGTAVYKVAEYARFVPIIADGGIQTGVHVVKALALGASTVMGSLAA 262
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 306 TRMVAGVGVPQITAVQVMSD-ALQDRIPLIADGGIRYSGDIGKALAGAAGSTVMIGGLFAG 364
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 263 TTEAPGVEYFSDGVRLLKRYGMSLDAKESSSQKRYFSGDKVK--IAQVSGSGTDK 320
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 365 TEEAPGDVELFOGRTYKSYRGMGLAAEK--GSKDRYFOEASDVLDKLPGEIGRVPYR 422
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 321 GSIQKFPYLIAGIQHCQDQIGARSLVLRSMYSGELKFEKRTMSAQIEGVH 374
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 423 GSVSGIVHQLMGLRATMGVYGVCATIEEMRT-----KPOFVKITGAGQGVESHVH 471
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 19
Q9KGN8 PRELIMINARY; PRT; 485 AA.
AC Q9KGN8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE INOSITOL-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205).
GN GUAB OR BH0020.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=96665;
RN [1]
RP "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL: AP001507; BAB03739.1; -.
DR HSP; P50099; IZPJ.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
```

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DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 485 AA; 52429 MW; DOB64489E5CF8B60 CRC64;

Query Match 32.1%; Score 628; DB 16; Length 485;
Best Local Similarity 32.2%; Pred. No. 4.7e-39;
Matches 155; Conservative 66; Mismatches 122; Indels 138; Gaps 5;

QY 28 DGLTYNDFLLPFGIDFIDAEVDLTSAITRKITLKTPLISSPMDVTVEADMAIAMAALMG 87
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 9 EGIITFDVLLVPAKSEVLPRDVSVKTKLTETLQNLPIISAGMDTYTEAKMAIAIEGG 68
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 88 IGFIHNCTPEFOANEVRKVK-----FDK----- 112
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 69 LGIHKNSVEEQAEQVDRVKRSESVITNPFELTPDRQVFEAHLGMKRYISGVPIVDE 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 113 ----- 112
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 129 DQKLVGILTNRLRFIEDYSTLIDDMVTENLVAPYGTTLKEAEILQKHIEKPLVD 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 113 ----- 112
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 189 ESGTLGLITIKDIEKVIETFPNSAKDSQGLIVGAAGVSAADTVRVAALVEAGVDVVI 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 144 DSSQGSNSVYQIAMVHIKQYKPHLVIGGNVYTAQAQKLNIDAGVDGLRVGMCGSGICIT 203
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 249 DTAHGSKGVLEKVKALIREQYPDLTIIAGNVATAEATRDLEAGANVVKVIGIPGSICT 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 204 QEVMACGRPQGTAVYKVAEYARFVPIIADGGIQTGVHVVKALALGASTVMGSLAA 263
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 309 RIVAGIGVPOITAVYDCANEARKHGVPIIADGGIKYSGSDIVKALAAAGHVMGLSLAGV 368
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 264 TEAPGEYFSDGVRLLKRYGMSLDAKESSSQKRYFSGDKVKIAQVSGSGIODKYSI 323
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 369 SESPEGEIEIFQGRQFQYKVRGMGLGAEK--GSKDRFQENNKLVPEGEGRIPIYKPL 426
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 324 QKVPYLIAGIQHCQDQIGARSLVLRSMYSGELKFEKRTMSAQIEG-GVHGLHSYEKR 382
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 427 HDTHQLVGGIRAGMGYCGTKTIDLR-----ENTQFTRITGAGLRESHPHDVQ 475
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 383 L 383
Db 476 I 476

RESULT 20
Q9JUD0 PRELIMINARY; PRT; 487 AA.
AC Q9JUD0;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PUTATIVE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205).
GN GUAB OR NMAL372.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holtroyd S.,
RA Jajels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
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"Complete DNA sequence of a serogroup A strain of *Neisseria*

meningitidis 22491";
 RA Nature 404:502-506(2000).
 RA EMBL; AL162755; CAB84618.1; -.
 DR HSSP; P49058; 1EEP.
 DR InterPro; IPR000644; CBS.
 DR InterPro; IPR003009; FMN_enzyme.
 DR InterPro; IPR001093; IMP_DH_GMP_RED.
 DR Pfam; PF00571; CBS; 2.
 DR Pfam; PF00478; IMPDH_C; 1.
 DR Pfam; PF01574; IMPDH_N; 1.
 DR SMART; SM00116; CBS; 2.
 DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
 DR Oxidoreductase; Complete proteome.
 KW OXIDOREDUCTASE; Complete proteome.
 SQ SEQUENCE 487 AA; 52367 MW; 984D41356B913BCB CRC64;

Query Match 32.0%; Score 626; DB 16; Length 487;
 Best Local Similarity 32.7%; Pred. No. 6.7e-39;
 Matches 155; Conservative 59; Mismatches 122; Indels 138; Gaps 6;

Qy 31 TYNDFLLPGFDFTADEVDLTSLTRKTKITLPLISSPMOTVTEADMAIAMLGGIGF 90
 Db 9 TDDVLLVPAHSTVLPDVKLTREITLNLPLLSAAMDVTTEARLAISNAQEGGIGI 68
 Qy 91 IHNCTPEQANEVRKVKFD-----
 Db 69 IHKNMPPENQARAIKVRHESGVVKKDPVTVAPTTLIREVLEMRQAKRKMSGLPVVENG 128
 Qy 112 -----
 Db 129 KVGIVTNRDLRFENRDLPSAINTPRELVTVPETGTSIDARELMHTHKVERVLVNE 188
 Qy 112 -----KT-----LLCGAAVGTREDDKYRLDLITQAGVDVIVD 144
 Db 189 KDEKGLITVKDILKTEFPNANKDSEGLRVGAAGVGGDTFEERVKALVEAGVDVIVD 248
 Qy 145 SQGNSVQIAMVHIKQYKPHLVGNVTAQAQKLNIDAGVGLRVGMCGGICITQ 204
 Db 249 TAGHSQGVDRVVRWKETYPHIQVIGNIAATAKALDLVAAGADAVKVGIGPGSICITR 308
 Qy 205 EVMACRPGGTAVYKVAEYARFVPIIADGGIQTGVHVVKALALGASTVMGSLAATT 264
 Db 309 IVAGVGVPLTAHNVAEALKGTGVPDIADGGIRFSGDIKALAAAGAYSVMLGGMFAGTE 368
 Qy 265 EAPGEYFFSDGVRLLKRYGMGSLDAMEKSSSSQKRYFSE---GDKVKIAQGVSGSIQDK 320
 Db 369 EAPGEIELYQGRSYKSYRGMSLGAM--SQGSADRYFQDKTDSADKY-VPEGIEGRVPYK 425
 Qy 321 GSIOKFPVPIYIAGIOHGGODICARSLSVLRSMYSSELKFKERTMSAQIEGGVH 374
 Db 426 GPIVNIHQLTGGLRSSMGYLGCAETAEHME-----KAEFVEITSAGMSSESHVH 474

RESULT 21
 Q9JZB5 PRELIMINARY; PRT; 487 AA.
 ID Q9JZB5
 AC Q9JZB5
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE IMP DEHYDROGENASE.
 GN NMB1201.
 OS *Neisseria meningitidis* (serogroup B).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; *Neisseria*.
 OX NCBI_TaxID=491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MC58 / SEROGROUP B;
 RX MEDLINE=20175755; PubMed=10710307;
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.F., Hickey E.K.,

HAFT D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 Mason T., Ciecko A., Parksey D.S., Blair E., Cittiore H., Clark E.B.,
 Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
 Gill J., Scarlato V., Masignani V., Pizsa M., Grandi G., Sun L.,
 Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,
 "Complete genome sequence of *Neisseria meningitidis* serogroup B strain
 MC58";
 RL Science 287:1809-1815(2000).
 DR EMBL; AE002468; AAF41583.1; -.
 DR HSSP; P49058; 1EEP.
 DR TIGR; NMB1201; -.
 DR InterPro; IPR000644; CBS.
 DR InterPro; IPR003009; FMN_enzyme.
 DR InterPro; IPR001093; IMP_DH_GMP_RED.
 DR Pfam; PF00571; CBS; 2.
 DR Pfam; PF00478; IMPDH_C; 1.
 DR Pfam; PF01574; IMPDH_N; 1.
 DR SMART; SM00116; CBS; 2.
 DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
 DR Oxidoreductase; Complete proteome.
 KW COMPLETE PROTEOME.
 SQ SEQUENCE 487 AA; 52383 MW; 4854B9C2681A2464 CRC64;

Query Match 32.0%; Score 625; DB 16; Length 487;
 Best Local Similarity 32.9%; Pred. No. 8e-39;
 Matches 156; Conservative 58; Mismatches 122; Indels 138; Gaps 6;

Qy 31 TYNDFLLPGFDFTADEVDLTSLTRKTKITLPLISSPMOTVTEADMAIAMLGGIGF 90
 Db 9 TDDVLLVPAHSTVLPDVKLTREITLNLPLLSAAMDVTTEARLAISNAQEGGIGI 68
 Qy 91 IHNCTPEQANEVRKVKFD-----
 Db 69 IHKNMPPENQARAVSKVRHESGVVKKDPVTVAPTTLIREVLEMRQAKRKMSGLPVVENG 128
 Qy 112 -----
 Db 129 KVGIVTNRDLRFENRDLPSAINTPRELVTVPETGTSIDARELMHTHKVERVLVNE 188
 Qy 112 -----KT-----LLCGAAVGTREDDKYRLDLITQAGVDVIVD 144
 Db 189 KDEKGLITVKDILKTEFPNANKDSEGLRVGAAGVGGDTFEERVKALVEAGVDVIVD 248
 Qy 145 SQGNSVQIAMVHIKQYKPHLVGNVTAQAQKLNIDAGVGLRVGMCGGICITQ 204
 Db 249 TAGHSQGVDRVVRWKETYPHIQVIGNIAATAKALDLVAAGADAVKVGIGPGSICITR 308
 Qy 205 EVMACRPGGTAVYKVAEYARFVPIIADGGIQTGVHVVKALALGASTVMGSLAATT 264
 Db 309 IVAGVGVPLTAHNVAEALKGTGVPDIADGGIRFSGDIKALAAAGAYSVMLGGMFAGTE 368
 Qy 265 EAPGEYFFSDGVRLLKRYGMGSLDAMEKSSSSQKRYFSE---GDKVKIAQGVSGSIQDK 320
 Db 369 EAPGEIELYQGRSYKSYRGMSLGAM--SQGSADRYFQDKTDSADKY-VPEGIEGRVPYK 425
 Qy 321 GSIOKFPVPIYIAGIOHGGODICARSLSVLRSMYSSELKFKERTMSAQIEGGVH 374
 Db 426 GPIVNIHQLTGGLRSSMGYLGCAETAEHME-----KAEFVEITSAGMSSESHVH 474

RESULT 22
 Q99WI9 PRELIMINARY; PRT; 488 AA.
 ID Q99WI9
 AC Q99WI9;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE INOSITOL-MONOPHOSPHATE DEHYDROGENASE.
 GN GUAB OR SA0375 OR SAV0390.
 OS *Staphylococcus aureus* (strain N315), and
Staphylococcus aureus (strain Mu50).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; *Staphylococcus*.

```
OX NCBI_TaxID=158879, 158878;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain N315), and S.aureus (strain Mu50);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekinizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240(2001).
DR ENBL; AP003130; BAB41602.1; -.
DR ENBL; AP003359; BAB56552.1; -.
DR HSSP; P50099; 1ZFU.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Complete proteome.
SQ SEQUENCE 488 AA; 52850 MW; C4E945D25D41491D CRC64;

Query Match 31.4%; Score 613; DB 16; Length 488;
Best Local Similarity 32.4%; Pred. No. 6.4e-38;
Matches 154; Conservative 59; Mismatches 129; Indels 134; Gaps 5;

QY 28 DGLTYNDFLILPGFDIADVDLTSALTTRKTKITLKTPLISSPMDTVEADMAIAMALMGG 87
DB 9 ESLTFDVLILPAOSDLIPKDVLSQVLSKVNIPVISAGMDTVTESKMAIAMARQGG 68
QY 88 IGFTHHCTPEFOANEYRKVK-
DB 69 LGVIHKMGVEEQADEVQVKRSENGVISNPFPLTPEESYAEALMKYRISGVPIVDN 128
QY 109 -----KFDK--- 112
DB 129 KEDRLVGLTNRDLRFEDFSIKIVDMTOENLITAPVNTLLEAEKILQKHRIEKLPL 188
QY 113 -----TLLCGAAGVTREDDKYRLDLLTOAGVDVIV 142
DB 189 VKDGRLEGLTIKDIEKVIETPPNAAKDEHGRLLVAAAIGISKDTDIRAKLVEAGVDVIV 248
QY 143 LSSQGSNVIQIAMVHIKQYPHLQVIGNVVTAQAQKNLIDAGVDGLRVGMCGSGTICI 202
DB 249 IDTAHGSKGVQIDQVKHKIKTYPETITLVAGNVATAETKDLFEAGADIVKVGIGPGSICT 308
QY 203 TOEWMACGRPGGTAVYKVAEYARFVGPIITADGGIQTGVHVVKALALGASTVMMGSLAA 262
DB 309 TRVAVGVGPQITAIYDCATEARKHGKAILADGGIKFSGDIKALAAGGHAVMLGSLLAG 368
QY 263 TTEAPGEFFSDGVRLLKRYRGMSLDAMEKSSSQKRYFSEGDVKV--IAQVSGSGTDK 320
DB 369 TEESPGATEIFQGRQYKYVRGMSLGAMEKGSND--RYFQEDKAPKRVFPEGIGRTAYK 426
QY 321 GSIQKFPYLIAGIOHGQCDIGARSLSVLRSMYSGLKFKFKRTMSAQIEGGVHGL 376
DB 427 GALQDTIYQLMGVRAGMGYTGSHDLRELRE-----EAQFTRMGPAGLAESHPHNI 477

RESULT 23
ID Q9RT87 PRELIMINARY; PRT; 500 AA.
AC Q9RT87;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE.
GN DR1878.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=RL;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans RL.";
RL Science 286:1571-1577(1999).
DR ENBL; AE002027; AAF11432.1; -.
DR HSSP; P49058; 1EEP.
DR TIGR; DR1878; -.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Complete proteome.
SQ SEQUENCE 500 AA; 53141 MW; 4351BC91B675A0D2 CRC64;

Query Match 31.0%; Score 606.5; DB 16; Length 500;
Best Local Similarity 30.7%; Pred. No. 2e-37;
Matches 145; Conservative 70; Mismatches 126; Indels 131; Gaps 4;

QY 28 DGLTYNDFLILPGFDIADVDLTSALTTRKTKITLKTPLISSPMDTVEADMAIAMALMGG 87
DB 25 EGITFDVLLQPRHSQVLPHEVDVSAQLTRVRLNIFVSAMDTVTETNMAIAMAREGG 84
QY 88 IGFTHHCTPEFOANEYRKVKKFDKTL-
DB 85 IGVVHKNSIDAQAEMIRKVKRSESGMIVDPTLPPSATVRDADRLMGEYRISGVPTAP 144
QY 116 ----- 115
DB 145 DGKLLGIITNRDMRFIDDLVPLGDVMTREHLVTPVPGTDLEQARELFKLNRIEKLIVTE 204
QY 116 -----CGAAVGTREDDKYRLDLLTOAGVDVIVLD 144
DB 205 GEYLRGLITIKDIEKSVKYPNAAKDDLGRLVAAAGVSADMDRAGALVORGADVLVD 264
QY 145 SSGNSVYQIAMVHIKQYPHLQVIGNVVTAQAQKNLIDAGVDGLRVGMCGSGICITQ 204
DB 265 SAHGHSQILNALSRVKEQF-DVDVIAGNVATRSRGARDLILAGADAVKVGIGPGSICITR 323
QY 205 EVMACGRPGGTAVYKVAEYARFVGPIITADGGIQTGVHVVKALALGASTVMMGSLAAT 264
DB 324 VVTGVGVQVTAIFEASAAAAMEAGIPVADGGIKQTGDVPKAIAAGASVVMGMSLAGTD 383
QY 265 EAPGEYFFSDGVRLLKRYRGMSLDAMEKSSSQKRYFSEGDVKVIAQGVSGSIQDKSIO 324
DB 384 EAPGETILRDGRRYKYSRGMSLGAMQGSAD--RYFGGSRKRVFPEGIGIIRGTAG 441
QY 325 KFPYLIAGIOHGQCDIGARSLSVLRSMYSGLKFKFKRTMSAQIEGGVHGL 376
DB 442 EVIYQFVGLKSSMGYCGAPDLTLRD-----TAQFVRITGASIVESHPHGV 488

RESULT 24
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Q9KWT3 ID Q9KWT3 PRELIMINARY; PRT; 489 AA.

AC Q9KWT3; 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE.

GN VC0767.

OS Vibrio cholerae.

OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.

OX NCBI_TaxID=666;

RP SEQUENCE FROM N.A.

RC STRAIN=EL TOR N16961 / SROTYPE 01;

RX MEDLINE=20406833; PubMed=10952301;

RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDaniel L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.

RA "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae."

RT cholerale.

RL Nature 406:477-483(2000).

DR EMBL; AE004162; AAF93932.1; -.

DR HSSP; P49058; 1EEP.

DR TIGR; VC0767; -.

DR InterPro; IPR006644; CBS.

DR InterPro; IPR003009; FMN_enzyme.

DR InterPro; IPR001093; IMP_DH_GMP_RED.

DR Pfam; PF00571; CBS; 2.

DR Pfam; PF00478; IMPDH_C; 1.

DR Pfam; PF01574; IMPDH_N; 1.

DR SMART; SM00116; CBS; 2.

DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.

KW Complete proteome.

SQ SEQUENCE 489 AA; 51942 MW; B38133B52F8661C4 CRC64;

Query Match 30.7%; Score 600; DB 16; Length 489;

Best Local Similarity 31.3%; Pred. No. 6.1e-37;

Matches 149; Conservative 68; Mismatches 121; Indels 138; Gaps 7;

QY 28 DGLTYNDFLILPGFIDFADDEVLTSLATKTKPLISSPMDTVEADMAIAMLGG 87

DB 9 EALTFDDVLVPAHSVLPNTADRLTKYLNALNPWSASMDTVEARLAIALAQEG 68

QY 88 IGFTHHNTPEFOANEVRKVKFDK----- 112

DB 69 IGFTHKMSIEQAAQVHVQKIEAGVTHPTVTRPTQTIADVMELTHYHGFAFPVTE 128

QY 113 ----- 112

DB 129 NNELVGITGRDVRFTDLTKSVAAVMTPKERLATYKEGATGAEOEKMKHARVEKILV 188

QY 113 -----TLCGAAVGTREDDKYRLDLLTQAGVDVIV 142

DB 189 NDEFQKGMTAKDFHAKESKPNACKDEOGRLEVRGAAGAAGNEERVALVEAGVDVUL 248

QY 143 LDSSQSNVYQIAMVHIKQYPHLOVIGNVVTAQAQNLIDAGVDGLRVGMCSSICIGI 202

DB 249 IDSSHGSEGVLRITRAAAYPHLEIIGNVATAGARALIEAGVSAYKVGIGPGSIC 308

QY 203 TQEWACGRPGQTAIVKAYEYARRFVPIADGGITGVHVKALALGASTVVMGSLLA 262

DB 309 TRIVTGVGPQITAIADAAGVANEYGIPIVADGGIRFSGDISKAATAAGASCVMVSMFAG 368

QY 263 TTEAPEYFSDGVRLLKRYKRGMSLDAMEKSSSKRYF---SEGDKVIAQVSGSIOD 319

DB 369 TEPAGEVILYQGRSKATVGMGSLGAMSGKSSD--RYFQTDNAADKL-VPEGIEGRY 425

QY 320 KGSIQRFVPLYIAGIHGQODI-GARSLSVLRSMYSGELKFEKRTMSAQIEGGVH 374

Db 426 KGHLEKIIHQMGGLR-SCMGLTGSATVEDLRT-----KAQFVRISGAGMKESHVH 475

RESULT 25

Q9PKM2 ID Q9PKM2 PRELIMINARY; PRT; 357 AA.

AC Q9PKM2; 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE, PUTATIVE.

GN TC0443.

OS Chlamydia muridarum.

OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

OX NCBI_TaxID=83560;

RP SEQUENCE FROM N.A.

RC STRAIN=MOPN / NIGG;

RX MEDLINE=20150255; PubMed=10684935;

RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.

RA "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39."

RT Nucleic Acids Res. 28:1397-1406(2000).

RL EMBL; AE002313; AAF39297.1; -.

DR HSSP; P12268; 1B30.

DR TIGR; TC0443; -.

DR InterPro; IPR003009; FMN_enzyme.

DR InterPro; IPR001093; IMP_DH_GMP_RED.

DR Pfam; PF00478; IMPDH_C; 1.

DR Pfam; PF01574; IMPDH_N; 1.

DR SMART; SM00116; CBS; 2.

DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.

KW Complete proteome.

SQ SEQUENCE 357 AA; 37642 MW; 3F191FC984BDA2A CRC64;

Query Match 30.7%; Score 599.5; DB 16; Length 357;

Best Local Similarity 38.6%; Pred. No. 4.2e-37;

Matches 135; Conservative 72; Mismatches 134; Indels 9; Gaps 3;

QY 28 DGLTYNDFLILPGFIDFADDEVLTSLATKTKPLISSPMDTVEADMAIAMLGG 87

DB 3 EALTFDDVLVPAHSVLPNTADRLTKYLNALNPWSASMDTVEARLAIALAQEG 62

QY 88 IGFTHHNTPEFOANEVRKVKFDKTLCCGAAVGTREDDKYRLDLLTQAGVDVIVLDSQ 147

DB 63 LGIVHKNDVNAQVAIVKQIKSQSTSSVIGGAVGIGQGLERAALVEAGIDTLVWDTAH 122

QY 148 GNSVYQIAMVHIKQYPHLOVIGNVVTAQAQNLIDAGVDGLRVGMCSSICITQEV 207

DB 123 GHSKLVLDLTAFTIRKNYP-VTLIVGNIVSKAALCLAEIGVDAYKVGIGPGSICITRIV 181

QY 208 ACGRPGQTAIVKAYEYARRFVPIADGGITGVHVKALALGASTVVMGSLLAATTEAP 267

DB 182 VGVLPLQTAIVMDVAEALHDSVRIADGGMYSGDIKVALAAGAHCVMLGSLMAGTDEAP 241

QY 268 GEYFFSDGVRLLKRYKRGMSLDAMEKSSSKRYFSEGDVKV-IAQVSGSIQDKGSIQK 326

DB 242 GEIVQINEHSYKMYRGMSLGAMKGS-ERYFQKNNAKFFVEGEGVLPYKGSGLHDV 299

QY 327 VPLYIAGIHGQODI-GARSLSVLRSMYSGELKFEKRTMSAQIEGGVHGL 376

DB 300 LYQILGGTRSGMVLGAHNLELRQ-----NAVESRITHSGRSESHIHL 344

Search completed: September 26, 2002, 08:28:17

Job time: 136 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2002, 08:27:41 ; Search time 32.37 Seconds
(without alignments)
1317.650 Million cell updates/sec

Title: US-09-853-918-30
Perfect score: 384
Sequence: 1 MADYLSIGGTGYVPEDGLTA.....MSAQIEGGVHGLSHYEKRLY 384

Scoring table: Oligo
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 11073796 residues

Word size : 0
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	146	38.0	604	22	ABG22269 Novel human diagno
2	66	17.2	66	22	ABG22265 Novel human diagno
3	55	14.3	55	22	ABG75199 Human colon cancer
4	31	8.1	514	11	AAR05432 Human IMPDH, Hom
5	31	8.1	514	11	AAR05431 Chinese hamster IM
6	24	6.2	217	21	AAB58491 Lung cancer associ
7	24	6.2	430	22	ABG23731 Novel human diagno
8	23	6.0	185	21	AAB58731 Breast and ovarian
9	23	6.0	215	22	ABG22268 Novel human diagno
10	23	6.0	287	22	ABG07490 Novel human diagno
11	23	6.0	537	22	ABB58547 Drosophila melanog

12	23	6.0	537	22	ABB65768 Drosophila melanog
13	22	5.7	161	21	AAG03970 Human secreted pro
14	21	5.5	371	20	AAG08965 A. gossypii inosin
15	20	5.2	155	22	ABG22266 Novel human diagno
16	18	4.7	156	22	ABG22267 Novel human diagno
17	14	3.6	95	22	AAO04552 Human polypeptide
18	14	3.6	151	20	AAG08964 A. gossypii inosin
19	13	3.4	403	22	AAG70679 S cerevisiae apopt
20	11	2.9	133	21	AAG27202 Zea mays protein f
21	11	2.9	140	21	AAG27201 Zea mays protein f
22	11	2.9	152	21	AAG27200 Zea mays protein f
23	11	2.9	435	21	AAG30890 Arabidopsis thalia
24	11	2.9	436	21	AAG43110 Arabidopsis thalia
25	11	2.9	443	21	AAG30889 Arabidopsis thalia
26	11	2.9	444	21	AAG43109 Arabidopsis thalia
27	11	2.9	502	21	AAG30888 Arabidopsis thalia
28	11	2.9	503	21	AAG43108 Arabidopsis thalia
29	10	2.6	436	21	AAG20991 Arabidopsis thalia
30	10	2.6	444	21	AAG20990 Arabidopsis thalia
31	10	2.6	503	21	AAG20989 Arabidopsis thalia
32	9	2.3	178	22	AAB80108 Corynebacterium gl
33	9	2.3	489	21	AAY97820 Pseudomonas sp. WF
34	9	2.3	506	22	AAG30418 C glutamicum prote
35	9	2.3	506	22	AAB80106 Corynebacterium gl
36	8	2.1	24	15	AAR89189 GPR adrenergic rec
37	8	2.1	24	15	AAR50808 G-protein coupled
38	8	2.1	24	17	AAW02740 G-protein coupled
39	8	2.1	86	20	AAY35259 Chlamydia pneumoni
40	8	2.1	139	21	AAG51650 Arabidopsis thalia
41	8	2.1	143	21	AAG11297 Arabidopsis thalia
42	8	2.1	143	21	AAG51977 Arabidopsis thalia
43	8	2.1	158	20	AAY41224 P. vulgaris YC43-P
44	8	2.1	164	21	AAG51649 Arabidopsis thalia
45	8	2.1	174	21	AAG51976 Arabidopsis thalia
46	8	2.1	177	21	AAG11296 Arabidopsis thalia
47	8	2.1	181	21	AAY86279 Human secreted pro
48	8	2.1	199	21	AAG11295 Arabidopsis thalia
49	8	2.1	264	22	ABG18250 Novel human diagno
50	8	2.1	307	22	AAU40893 Propionibacterium
51	8	2.1	308	21	AAG09005 Arabidopsis thalia
52	8	2.1	308	21	AAY86502 Human gene 65-enco
53	8	2.1	325	22	AAU35218 Enterococcus faeca
54	8	2.1	325	22	AAU35950 Helicobacter pylor
55	8	2.1	327	22	AAU33399 Enterococcus faeca
56	8	2.1	328	22	AAU37668 Streptococcus pneu
57	8	2.1	348	21	AAG09004 Arabidopsis thalia
58	8	2.1	348	21	AAG17828 Arabidopsis thalia
59	8	2.1	349	21	AAG31216 Arabidopsis thalia
60	8	2.1	362	21	AAG31215 Arabidopsis thalia
61	8	2.1	367	21	AAG09003 Arabidopsis thalia
62	8	2.1	367	21	AAG17827 Arabidopsis thalia
63	8	2.1	368	21	AAG31214 Arabidopsis thalia
64	8	2.1	386	21	AAG17826 Arabidopsis thalia
65	8	2.1	473	21	AAB42135 Human ORFX ORF1899
66	8	2.1	479	21	AAB29656 Human membrane-ass
67	8	2.1	479	22	AAB97000 Oesophagus cancer
68	8	2.1	481	19	AAY11109 H. pylori ORF hp8e
69	8	2.1	481	19	AAW98634 Murine zalpha30 po
70	8	2.1	700	22	AAU00956 H11 binding site c
71	7	1.8	7	22	AAW45268 H11 binding site c
72	7	1.8	7	22	AAW45273 H11 binding site c
73	7	1.8	7	22	AAW45278 H11 binding site c
74	7	1.8	7	22	AAW45283 A metalloprotease
75	7	1.8	32	20	AAW68536 NlpD repeat sequen
76	7	1.8	44	20	AAU14005 Propionibacterium
77	7	1.8	57	22	AAU67995 Human haematologic
78	7	1.8	60	22	AAU80321 Propionibacterium
79	7	1.8	61	22	AAU48738 Propionibacterium
80	7	1.8	65	22	AAU55029 Propionibacterium
81	7	1.8	67	22	AAW62708 Human immune/haema
82	7	1.8	71	21	AAG24493 Arabidopsis thalia
83	7	1.8	71	21	AAG38103 Arabidopsis thalia
84	7	1.8	72	22	AAB70019 Mammalian CD4 IL-1

85 7 1.8 77 21 AAG24492 Arabidopsis thalia
86 7 1.8 78 21 AAG38102 Arabidopsis thalia
87 7 1.8 115 22 AAG91827 C glutamicum prote
88 7 1.8 126 20 AAY12621 Human 5' EST seque
89 7 1.8 129 21 AAG17469 Arabidopsis thalia
90 7 1.8 135 21 AAG17468 Arabidopsis thalia
91 7 1.8 139 21 AAG17467 Arabidopsis thalia
92 7 1.8 142 21 AAG24491 Arabidopsis thalia
93 7 1.8 143 21 AAG38101 Arabidopsis thalia
94 7 1.8 148 21 AAG05976 Arabidopsis thalia
95 7 1.8 149 22 AAM80713 Human haematologic
96 7 1.8 153 22 AAM80008 Corynebacterium gl
97 7 1.8 155 22 AAM81278 Human haematologic
98 7 1.8 157 22 AAG89983 C glutamicum prote
99 7 1.8 158 22 AAB80107 Corynebacterium gl
100 7 1.8 165 20 AAY50044 Rhodobacter sphaer

ALIGNMENTS

RESULT 1
ABG22269
ID ABG22269 standard; Protein: 604 AA.
XX
AC ABG22269;

XX
DT 18-FEB-2002 (first entry)

XX
DE Novel human diagnostic protein #22260.

XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX
OS Homo sapiens.

XX
PN WO200175067-A2.

XX
PD 11-OCT-2001.

XX
PF 30-MAR-2001; 2001WO-US08631.

XX
PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX
PA (HYSE-) HYSEQ INC.

XX
PI Drmanac RT, Liu C, Tang YT;

XX
PD WPI; 2001-639362/73.

DR N-PSDB; AAS86456.

XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

XX
PS Claim 20; SEQ ID No 52628; 103pp; English.

XX
PT The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (II) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 604 AA;

Query Match 38.0%; Score 146; DB 22; Length 604;
Best Local Similarity 100.0%; Pred. No. 3.6e-136;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 AEYARFGVPILADGGIQTGVHVVKALALGASTVMGMSLLAATTEAPGEYFFSDGVRLKK 280
|||||

Db 441 aeyarirfvpiladggigtgvhvkvkaiagastvmgmsllaatteapgeyffsdgvrllk 500
|||||

QY 281 YRGMGSLDAMEKSSSQKRYFSEGDVKVIAQGVSGSIQDKGSIQKFPVPLIAGIQHGCQD 340
|||||

Db 501 yrgmsldameksssqkryfsegdvkviagqvgsgsiqdkgsiqkfvpyliagiqhgcd 560
|||||

QY 341 IGARSLSVLRSMYSGELKFEKRTMS 366
|||||

Db 561 igarslsvlrsmymysgelkfekrms 586
|||||

RESULT 2

ABG22265
ID ABG22265 standard; Protein: 66 AA.

XX
AC ABG22265;

XX
DT 18-FEB-2002 (first entry)

XX
DE Novel human diagnostic protein #22256.

XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

XX
PN WO200175067-A2.

XX
PD 11-OCT-2001.

XX
PF 30-MAR-2001; 2001WO-US08631.

XX
PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX
PA (HYSE-) HYSEQ INC.

XX
PI Drmanac RT, Liu C, Tang YT;

XX
PD WPI; 2001-639362/73.

DR N-PSDB; AAS86452.

XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

XX
PS Claim 20; SEQ ID No 52624; 103pp; English.

XX
PT The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 66 AA;

Query Match 17.2%; Score 66; DB 22; Length 66;
 Best Local Similarity 100.0%; Pred. No. 1.4e-57;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 DKGSTQKFPVYLIAGTQHCQDIGARSLVLRSMYSGLKFEKRTMSAQIEGGVHGLHS 378

Db 1 dkgsiqkrtvpyliagiqhgcqdigarslvlrsmysgelkfekrtsaqieggvghlgs 60

QY 379 YEKRLY 384

Db 61 yekrly 66

RESULT 3

AAAG75199
 ID AAG75199 standard; Protein; 55 AA.

XX AC AAG75199;

XX DT 03-SEP-2001 (first entry)

XX DE Human colon cancer antigen protein SEQ ID NO:5963.

XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;

XX KW colorectal carcinoma; chromosome 7.

XX OS Homo sapiens.

XX PN WO200122920-A2.

XX PD 05-APR-2001.

XX PF 28-SEP-2000; 2000WO-US26524.

XX PR 29-SEP-1999; 98US-0157137.

XX PR 03-NOV-1999; 99US-0163280.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Birse CE, Rosen CA;

XX DR WPI; 2001-235357/24.

XX DR N-PSDB; AAH34604.

XX PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 XX useful for preventing, diagnosing and/or treating colorectal cancers -

XX PS Claim 11; Page 7468-7469; 9803pp; English.

XX CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P

CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the patients own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated Ps,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC and AAB77789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.

XX Sequence 55 AA;

Query Match 14.3%; Score 55; DB 22; Length 55;
 Best Local Similarity 100.0%; Pred. No. 9.8e-47;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 330 LIAGTQHCQDIGARSLVLRSMYSGLKFEKRTMSAQIEGGVHGLHSYEKRLY 384

Db 1 liagiqhgcqdigarslvlrsmysgelkfekrtsaqieggvghlgsyekrly 55

RESULT 4

AAAR05432
 ID AAR05432 standard; protein; 514 AA.

XX AC AAR05432;

XX DT 31-AUG-1990 (first entry)

XX DE Human IMPDH.

XX KW Inosine 5'-mono-phosphate dehydrogenase; hepatomas;
 XX guanosine monophosphate.

XX OS Homo sapiens.

XX PN WO9001545-A.

XX PD 22-FEB-1990.

XX PF 02-AUG-1989; 89WO-0000344.

XX PR 12-AUG-1988; 88US-0232302.

XX PA (ARCH-) ARCH. DEV. CORP.

XX PI Collart FR, Huberman E;

XX DR WPI; 1990-083504/11.

XX DR P-PSDB; AAR05432.

XX PT DNA encoding eukaryotic inosine 5'-mono-phosphate dehydrogenase -
 XX used to detect high levels of enzyme activity of tumour cells,
 XX esp. hepatomas, and to produce guanosine monophosphate.

XX PS Claim 8; Fig 1; 51pp; English.

XX CC A 35 aa segment corresponds to deduced aa residues 336-370 in
 XX both the human and Chinese hamster proteins.

XX CC See also AAQ03541.

XX Sequence 514 AA;

Query Match 8.1%; Score 31; DB 11; Length 514;

Best Local Similarity 100.0%; Pred. No. 5.5e-22;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGASTVMGSLLAATTEAPGEYFFSDG 275
Db 375 kalgastvmmgslaatteapgeyffsdg 405

RESULT 5
AAR05431
ID AAR05431 standard; protein; 514 AA.
XX AC AAR05431;
XX DT 31-AUG-1990 (first entry)
XXR Chinese hamster IMPDH.
XX DE
XX KW Inosine 5'-mono-phosphate dehydrogenase; hepatomas;
KW guanosine monophosphate.
XX Cricetulus sp.
OS WO9001545-A.
PN 22-FEB-1990.
PD
XX 02-AUG-1989; 89WO-0000344.
XX 12-AUG-1988; 88US-0232302.
XX (ARCH-) ARCH. DEV. CORP.
XX Collart FR, Huberman E;
XX WPI; 1990-083504/11.
DR N-PSDB; AAQ03541.
XX DNA encoding eukaryotic inosine 5'-mono-phosphate dehydrogenase -
PT used to detect high levels of enzyme activity of tumour cells,
PT esp. hepatomas, and to produce guanosine monophosphate.
XX Claim 8; Fig 2; 51pp; English.
PS A 35 aa segment corresponds to deduced aa residues 336-370 in
CC both the human and Chinese hamster proteins.
CC See also AAQ03540.
XX Sequence 514 AA;

Query Match 8.1%; Score 31; DB 11; Length 514;
Best Local Similarity 100.0%; Pred. No. 5.5e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGASTVMGSLLAATTEAPGEYFFSDG 275
Db 375 kalgastvmmgslaatteapgeyffsdg 405

RESULT 6
AAB58491
ID AAB58491 standard; protein; 217 AA.
XX AC AAB58491;
XX DT 14-MAR-2001 (first entry)
XX DE Lung cancer associated polypeptide sequence SEQ ID 829.
XX Human; lung cancer associated protein; neuroprotective; cytostatic;
KW cardioactive; immunomodulatory; muscular active; vulnerary;
KW gastrointestinal; nephrotropic; antiinfective; gynecological;
KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
KW proliferative disorder; wound healing; infectious disease.

OS Homo sapiens.
PN WO200055180-A2.
XX 21-SEP-2000.
XX 08-MAR-2000; 2000WO-US05918.
XX 12-MAR-1999; 99US-0124270.
XX (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX Ruben SM;
XX WPI; 2000-587514/55.
DR N-PSDB; AAF18367.
XX Lung cancer associated gene sequences, referred to as lung cancer
PT antigens, useful for treatment, prevention, and diagnosis of disorders
PT such as lung cancer -
XX Claim 11; Page 1370-1371; 1425pp; English.
XX Polynucleotide sequences AAF1982 - AAF18424 encode human lung cancer
CC associated proteins represented in AAB58106 - AAB58548. Lung cancer
CC associated proteins and polynucleotide sequences, their agonists, and
CC antagonists may have neuroprotective; cytostatic; cardioactive;
CC immunomodulatory; muscular active general; vulnerary; gastrointestinal
CC general; nephrotropic; antiinfective; gynecological; or antibacterial
CC activity. The invention also includes antibodies specific for the
CC protein or polynucleotide sequences. The lung cancer associated
CC polynucleotide sequences may be used for detection of lung cancer,
CC chromosome identification, as chromosome markers, and for numerous other
CC diagnostic or research purposes. The proteins may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders. The proteins may also be used in the treatment of wounds and
CC infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and
CC peptide AAB58549 are used in the course of the invention for the
CC identification and characterisation of the polynucleotide and protein
CC sequences.
XX Sequence 217 AA;

Query Match 6.2%; Score 24; DB 21; Length 217;
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 GGIGFIHNNCTPEFQANEVRKVK 109
Db 50 ggigfihnnctpefqanevrkvk 73

RESULT 7
ABG23731
ID ABG23731 standard; protein; 430 AA.
XX AC ABG23731;
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #23722.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX Homo sapiens.
OS WO200175067-A2.
PN 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.
 XX PF
 XX 31-MAR-2000; 2000US-0540217.
 XX PR
 XX 23-AUG-2000; 2000US-0649167.
 XX PR
 XX (HYSE-) HYSEQ INC.
 XX PA
 XX Drmanac RT, Liu C, Tang YT;
 XX PI
 XX WPI: 2001-639362/73.
 XX DR
 XX N-PSDB; AAS87918.
 XX
 XX New isolated polynucleotide and encoded polypeptides, useful in
 XX diagnostics, forensics, gene mapping, identification of mutations
 XX responsible for genetic disorders or other traits and to assess
 XX biodiversity -
 XX
 XX Claim 20; SEQ ID No 54090; 103pp; English.
 XX
 XX The invention relates to isolated polynucleotide (I) and
 XX polypeptide (II) sequences. (I) is useful as hybridisation probes.
 XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 XX and gene mapping, and in recombinant production of (II). The
 XX polynucleotides are also used in diagnostics as expressed sequence tags
 XX for identifying expressed genes. (I) is useful in gene therapy techniques
 XX to restore normal activity of (II) or to treat disease states involving
 XX (II). (II) is useful for generating antibodies against it, detecting or
 XX quantitating a polypeptide in tissue, as molecular weight markers and as
 XX a food supplement. (II) and its binding partners are useful in medical
 XX imaging of sites expressing (II). (I) and (II) are useful for treating
 XX disorders involving aberrant protein expression or biological activity.
 XX The polypeptide and polynucleotide sequences have applications in
 XX diagnostics, forensics, gene mapping, identification of mutations
 XX responsible for genetic disorders or other traits to assess biodiversity
 XX and to produce other types of data and products dependent on DNA and
 XX amino acid sequences. ABG00010-ABG30377 represent novel human
 XX diagnostic amino acid sequences of the invention.
 XX Note: The sequence data for this patent did not appear in the printed
 XX specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 430 AA;
 XX
 XX Query Match 6.2%; Score 24; DB 22; Length 430;
 XX Best Local Similarity 100.0%; Pred. No. 4.2e-15;
 XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 MADYLISSGTYGYPEDGLTAQQLF 24
 XX |
 XX Db 9 madyliisgtygypedgltaqqlf 32
 XX
 XX RESULT 8
 XX AAB58731
 XX ID AAB58731 standard; Protein; 185 AA.
 XX AC AAB58731;
 XX DT 27-MAR-2001 (first entry)
 XX
 XX Breast and ovarian cancer associated antigen protein sequence SEQ ID 439.
 XX
 XX Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
 XX neurotropic; neuroprotective; antiviral; antitumorigenic; hepatotropic;
 XX antidiabetic; antiinflammatory; antitumor; antitumor; antitumor;
 XX antitumor; antitumor; antitumor; antitumor; antitumor;
 XX Addison's disease; allergy; autoimmune haemolytic anaemia;
 XX autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
 XX multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
 XX cardiovascular disorder; wound healing; neurological disease.
 XX

OS Homo sapiens.
 XX
 XX PN WO2000055173-A1.
 XX
 XX PD 21-SEP-2000.
 XX
 XX PF 08-MAR-2000; 2000WO-US05881.
 XX
 XX PR 12-MAR-1999; 99US-0124270.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX PI Rosen CA, Ruben SM;
 XX
 XX PT WPI: 2000-611515/58.
 XX
 XX DR N-PSDB; AAF21634.
 XX
 XX PT New human breast and ovarian cancer associated gene sequences and the
 XX polypeptides encoded by these genes, useful in the prevention,
 XX treatment and diagnosis of cancer, immune disorders, cardiovascular
 XX disorders and neurological diseases -
 XX
 XX PS Claim 11; Page 865-866; 1299pp; English.
 XX
 XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
 XX proteins AAB58711 - AAB59128. The DNA and protein sequences are
 XX associated with breast and ovarian cancer. Included in the invention are
 XX sequences AAF22032 - AAF22040 and AAB59129 which are used in the
 XX isolation and characterisation of the DNA and protein sequences of the
 XX invention. The breast and ovarian cancer associated DNA, protein, agonist
 XX or antagonist sequences exhibit cytostatic; immunosuppressive;
 XX neurotropic; neuroprotective; antiviral; antitumorigenic; hepatotropic;
 XX antidiabetic; antiinflammatory; antitumor; antitumor; antitumor;
 XX antibacterial; antifungal; antiparasitic and cardiant activity. The
 XX polynucleotide and protein sequences are used in the diagnosis of cancer,
 XX particularly breast and ovarian cancer. The nucleic acid sequences,
 XX proteins, agonists and antagonists may also be used in the diagnosis,
 XX prevention and treatment of immune disorders e.g. Addison's disease,
 XX allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
 XX diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 XX arthritis and ulcerative colitis; cardiovascular disorders such as
 XX myocardial ischaemias; wound healing; neurological diseases such as
 XX cerebral anoxia and epilepsy; and infectious diseases.
 XX
 XX SQ Sequence 185 AA;
 XX
 XX Query Match 6.0%; Score 23; DB 21; Length 185;
 XX Best Local Similarity 100.0%; Pred. No. 1.9e-14;
 XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 167 LQVIGGNVTVTAQAQKNIIDAGVD 189
 XX |
 XX Db 98 lqviggnvvttaqaqknliidagvd 120
 XX
 XX RESULT 9
 XX ABG22268
 XX ID ABG22268 standard; Protein; 215 AA.
 XX AC ABG22268;
 XX DT 18-FEB-2002 (first entry)
 XX
 XX Novel human diagnostic protein #22259.
 XX
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO200175067-A2.
 XX

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PD XX 11-OCT-2001.
PF XX
PR XX 30-MAR-2001; 2001WO-US08631.
PR XX
PR XX 31-MAR-2000; 2000US-0540217.
PR XX
PR XX 23-AUG-2000; 2000US-0649167.
PR XX
PA (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
PI
XX WPI: 2001-639362/73.
DR N-PSDB; AAS86455.
DR
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 20; SEQ ID No 52627; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 215 AA;

Query Match 6.0%; Score 23; DB 22; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.2e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 AIAMALMGIGIFHHNCTPEFQA 101
Db 4 aliamalmgigifhnhctpefqa 26

RESULT 10
ABG07490
ID ABG07490 standard; Protein; 287 AA.
XX
XX ABG07490;
AC
XX
XX DT 13-FEB-2002 (first entry)
XX
XX DE Novel human diagnostic protein #7481.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensics;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
OS
XX
XX WO200175067-A2.
PN
XX
XX 11-OCT-2001.
PD

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XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
PR
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
PA
XX
XX Drmanac RT, Liu C, Tang YT;
PI
XX WPI: 2001-639362/73.
DR N-PSDB; AAS71677.
DR
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 20; SEQ ID No 37849; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 287 AA;

Query Match 6.0%; Score 23; DB 22; Length 287;
Best Local Similarity 100.0%; Pred. No. 2.8e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 AIAMALMGIGIFHHNCTPEFQA 101
Db 76 aliamalmgigifhnhctpefqa 98

RESULT 11
ABB58547
ID ABB58547 standard; Protein; 537 AA.
XX
XX ABB58547;
AC
XX
XX DT 26-MAR-2002 (first entry)
XX
XX DE Drosophila melanogaster polypeptide SEQ ID NO 2433.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
XX Drosophila melanogaster.
OS
XX
XX WO200171042-A2.
PN
XX
XX 27-SEP-2001.
PD
XX

```

PF 23-MAR-2001; 2001WO-US09231.
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 PA
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 XX N-PSDB; ABL02650.
 DR
 DR New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PT
 XX Disclosure; SEQ ID NO 2433; 21pp + Sequence Listing; English.
 PS
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 537 AA;

Query Match 6.0%; Score 23; DB 22; Length 537;
 Best Local Similarity 100.0%; Pred. No. 5.1e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 EAPGEYFFSDGVRLKKYRGMGSL 287
 ||||||||||||||||||
 Db 414 eapgeyffsdgvrlkkymgmsl 436

RESULT 12
 ABB65768
 ID ABB65768 standard; Protein; 537 AA.
 XX
 AC ABB65768;

XX 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 24096.
 XX
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 PI
 XX WO200171042-A2.
 PD
 PD 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 PA
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 XX N-PSDB; ABL09871.
 DR
 XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 XX Disclosure; SEQ ID NO 24096; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 537 AA;

Query Match 6.0%; Score 23; DB 22; Length 537;
 Best Local Similarity 100.0%; Pred. No. 5.1e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 EAPGEYFFSDGVRLKKYRGMGSL 287
 ||||||||||||||||||
 Db 414 eapgeyffsdgvrlkkymgmsl 436

RESULT 13
 AAG03970
 ID AAG03970 standard; Protein; 161 AA.
 XX
 AC AAG03970;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 XX Human secreted protein, SEQ ID NO: 8051.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 PD
 PD 06-SEP-2000.

XX 21-FEB-2000; 2000EP-0200610.
 XX
 PR 26-FEB-1999; 99US-0122487.
 XX (GEST) GENSET.
 PA
 XX Dumas Milne Edwards J, Duclert A, Giordano J;
 PI
 XX WPI; 2000-500381/45.
 DR N-PSDB; AAC03976.
 DR
 XX

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 XX Claim 13; SEQ ID 8051; 71pp + CD-ROM; English.

XX The present sequence is a polypeptide encoded by one of a large number
 CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
 CC were prepared from total human RNAs or polyA+ RNAs derived from 30
 CC different tissues. EST sequences usually correspond mainly to the 3'
 CC untranslated region (UTR) of the mRNA because they are often obtained
 CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
 CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in

CC those cases where longer cDNA sequences have been obtained, the full 5'
CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
CC ends and can therefore be used to obtain full length cDNAs and genomic
CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
CC chromosome mapping procedures. They are used to obtain upstream
CC regulatory sequences and to design expression and secretion vectors.
XX
SQ Sequence 161 AA;

Query Match 5.7%; Score 22; DB 21; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 GGIGFIHHNCTPEFOANEVRKV 107
|||||
DB 86 ggigfihhnmctpefqanevrkv 107

RESULT 14
AAV08965
ID AAY08965 standard; Protein; 371 AA.

XX AC AAY08965;

XX DT 19-AUG-1999 (first entry)

DE A. gossypii inosine-monophosphate dehydrogenase protein fragment 2.

XX Purine biosynthesis; phosphoribosylpyrophosphate synthetase; KPR1; KPR2;
KW glutamine-phosphoribosylpyrophosphate amidotransferase; ADE4; GUA1;
KW IMP-dehydrogenase; GUA1; GMP-synthetase; GUA2; PRPP synthetase; mouth;
KW riboflavin; vitamin B2; treatment; inflammation; throat; mucosal layer;
KW skin disorder.

XX AShbaya gossypii.

XX EP927761-A2.

XX PD 07-JUL-1999.

XX PF 08-DEC-1998; 98EP-0123331.

XX PR 23-DEC-1997; 97DE-1057755.

XX PA (BADI) BASF AG.

XX Hoeffken HW, Jimenez A, Pompejus M, Revuelta Doval JL;
PI Santos Garcia MA, Seuilberger H;

XX WPI; 1999-373465/32.

XX N-PSDB; AAX78081.

XX AShbaya gossypii purine biosynthesis enzymes and related genes for
PT production of riboflavin

XX Claim 13; Page 33-34; 48pp; German.

XX This invention describes novel enzymes involved in purine biosynthesis
CC in Ashbaya gossypii. The enzymes described in the invention include
CC Phosphoribosylpyrophosphate (PRPP) synthetases KPR1 and KPR2
CC glutamine-phosphoribosylpyrophosphate amidotransferase (ADE4)
CC IMP-dehydrogenase (GUA1) and a GMP-synthetase (GUA2). The nucleic acid
CC sequences encoding the enzymes involved in purine biosynthesis are used
CC to genetically modify microorganisms, for the production of riboflavin.
CC Riboflavin, also known as vitamin B2, is essential in humans and animals
CC and is used to treat inflammation of the mouth and throat mucosal layer
CC as well as inflammation in skin disorders. This sequence represents a
CC fragment of the inosine-monophosphate dehydrogenase protein encoded by
CC the GUA1 gene represented in AAX78081.

XX Sequence 371 AA;

Query Match 5.5%; Score 21; DB 20; Length 371;
Best Local Similarity 100.0%; Pred. No. 3.5e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 GSICITQEVNACGRPGGTAVY 218
|||||
DB 180 gsicitqevnmacgrpggtavy 200

RESULT 15
ABG22266
ID ABG22266 standard; Protein; 155 AA.

XX AC ABG22266;

XX DT 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #22257.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS86453.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

XX Claim 20; SEQ ID No 52625; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAG00010-AAG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: the sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 155 AA;

	Query Match	5.2%; Score 20; DB 22; Length 155;	
	Best Local Similarity	100.0%; Pred. No. 1.5e-11;	
	Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	29 GLTYNDFLILPGFIDFIAD 48		
DB	23 gltyndflilpgfidfiade 42		
	RESULT 16		
ID	ABG222267		
XX	ABG222267 standard; Protein; 156 AA.		
AC	ABG222267;		
DT	18-FEB-2002 (first entry)		
DE	Novel human diagnostic protein #22258.		
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;		
KW	food supplement; medical imaging; diagnostic; genetic disorder.		
OS	Homo sapiens.		
PX	WO200175067-A2.		
PN	11-OCT-2001.		
PD	30-MAR-2001; 2001WO-US08631.		
PF	31-MAR-2000; 2000US-0540217.		
PR	23-AUG-2000; 2000US-0649167.		
PA	(HYSE-) HYSEQ INC.		
PI	Dzmanac RT, Liu C, Tang YT;		
DR	WPI; 2001-639362/73.		
N-PSDB;	AAS86454.		
PT	New isolated polynucleotide and encoded polypeptides, useful in		
PT	diagnostics, forensics, gene mapping, identification of mutations		
PT	responsible for genetic disorders or other traits and to assess		
PT	biodiversity -		
XX	Claim 20; SEQ ID NO 52626; 103pp; English.		
CC	The invention relates to isolated polynucleotide (I) and		
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,		
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome		
CC	and gene mapping, and in recombinant production of (II). The		
CC	polynucleotides are also used in diagnostics as expressed sequence tags		
CC	for identifying expressed genes. (I) is useful in gene therapy techniques		
CC	to restore normal activity of (II) or to treat disease states involving		
CC	(II). (II) is useful for generating antibodies against it, detecting or		
CC	quantitating a polypeptide in tissue, as molecular weight markers and as		
CC	a food supplement. (II) and its binding partners are useful in medical		
CC	imaging of sites expressing (II). (I) and (II) are useful for treating		
CC	disorders involving aberrant protein expression or biological activity.		
CC	The polypeptide and polynucleotide sequences have applications in		
CC	diagnostics, forensics, gene mapping, identification of mutations		
CC	responsible for genetic disorders or other traits to assess biodiversity		
CC	and to produce other types of data and products dependent on DNA and		
CC	amino acid sequences. ABG00010-ABG30377 represent novel human		
CC	diagnostic amino acid sequences of the invention.		
CC	Note: The sequence data for this patent did not appear in the printed		
CC	specification, but was obtained in electronic format directly from WIPO		
CC	at ftp.wipo.int/pub/published_pct_sequences.		
XX	Sequence 156 AA;		
SQ			
Query Match	4.7%; Score 18; DB 22; Length 156;		
Best Local Similarity	100.0%; Pred. No. 1.5e-11;		
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	29 GLTYNDFLILPGFIDFIAD 48		
DB	23 gltyndflilpgfidfiade 42		
	RESULT 17		
ID	AAO04552		
XX	AAO04552 standard; Protein; 95 AA.		
AC	AAO04552;		
DT	06-NOV-2001 (first entry)		
DE	Human polypeptide SEQ ID NO 18444.		
XX	Human; cytokine; cell proliferation; cell differentiation; gene therapy;		
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;		
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;		
KW	nervous system disorders; arthritis; inflammation.		
OS	Homo sapiens.		
XX	WO200164835-A2.		
PN	07-SEP-2001.		
PD	26-FEB-2001; 2001WO-US04927.		
PF	28-FEB-2000; 2000US-0515126.		
PR	18-MAY-2000; 2000US-0577409.		
PA	(HYSE-) HYSEQ INC.		
PI	Tang YT, Liu C, Drmanac RT;		
DR	WPI; 2001-514838/56.		
N-PSDB;	AAI844483.		
PT	Isolated nucleic acids and polypeptides, useful for preventing		
PT	diagnosing and treating e.g. leukaemia, inflammation and immune		
PT	disorders -		
XX	Claim 20; SEQ ID NO 18444; 1399pp + Sequence Listing; English.		
CC	The invention relates to human polynucleotides (AI179941-AA193841) and		
CC	the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to		
CC	cytokine, cell proliferation or cell differentiation or which may induce		
CC	production of other cytokines in other cell populations. The		
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or		
CC	peptide therapy. The polypeptides have various cytokine-like activities,		
CC	e.g. stem cell growth factor activity, haematopoiesis regulating		
CC	activity, tissue growth factor activity, immunomodulatory activity and		
CC	activin/inhibin activity and may be useful in the diagnosis and/or		
CC	treatment of cancer, leukaemia, nervous system disorders, arthritis and		
CC	inflammation.		
CC	Note: The sequence data for this patent did not form part of the printed		
CC	specification, but was obtained in electronic format directly from WIPO		
CC	at ftp.wipo.int/pub/published_pct_sequences.		
XX	Sequence 95 AA;		
SQ			
Query Match	3.6%; Score 14; DB 22; Length 95;		
Best Local Similarity	100.0%; Pred. No. 8.9e-06;		
Matches	14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	86 GGIGFHHNCTPEF 99		
DB	61 ggigfhhnctpef 74		

RESULT 18
AAY08964
ID AAY08964 standard; Protein; 151 AA.
XX
AC AAY08964;
XX
DT 19-AUG-1999 (first entry)
XX
DE A. gossypii inosine-monophosphate dehydrogenase protein fragment 1.
XX
KW Purine biosynthesis; phosphoribosylpyrophosphate synthetase; KPR1; KPR2;
KW glutamine-phosphoribosylpyrophosphate amidotransferase; ADE4; GUA1;
KW IMP-dehydrogenase; GUA1; GMP-synthetase; GUA2; PRPP synthetase; mouth;
KW riboflavin; vitamin B2; treatment; inflammation; throat; mucosal layer;
KW skin disorder.
XX
OS Ashbya gossypii.
XX
PN EP927761-A2.
XX
PD 07-JUL-1999.
XX
PF 08-DEC-1998; 98EP-0123331.
XX
PR 23-DEC-1997; 97DE-1057755.
XX
PA (BADI) BASF AG.
XX
PI Hoeffken HW, Jimenez A, Pompejus M, Revuelta Doval JL;
PI Santos Garcia MA, Seulberger H;
XX
DR N-PSDB; AAX78081.
XX
PT Ashbya gossypii purine biosynthesis enzymes and related genes for
PT production of riboflavin
XX
PS Claim 13; Page 32-33; 48pp; German.
XX
CC This invention describes novel enzymes involved in purine biosynthesis
CC in Ashbya gossypii. The enzymes described in the invention include
CC Phosphoribosylpyrophosphate (PRPP) synthetases KPR1 and KPR2
CC glutamine-phosphoribosylpyrophosphate amidotransferase (ADE4)
CC IMP-dehydrogenase (GUA1) and a GMP-synthetase (GUA2). The nucleic acid
CC sequences encoding the enzymes involved in purine biosynthesis are used
CC to genetically modify microorganisms, for the production of riboflavin.
CC Riboflavin, also known as vitamin B2, is essential in humans and animals
CC and is used to treat inflammation of the mouth and throat mucosal layer
CC as well as inflammation in skin disorders. This sequence represents a
CC fragment of the inosine-monophosphate dehydrogenase protein encoded by
CC the GUA1 gene represented in AAX78081.
XX
SQ Sequence 151 AA;

Query Match 3.6%; Score 14; DB 20; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SSPMDTVTEADMAI 80
Db 73 sspmdtvteadmai 86
|||||

RESULT 19
AAG70679
ID AAG70679 standard; Protein; 403 AA.
XX
AC AAG70679;
XX
DT 27-JUL-2001 (first entry)
XX

DE S cerevisiae apoptosis associated protein YAR073W.
XX
KW Yeast; fungus; apoptosis; infection; proliferative disease;
KW vaccine; autoimmune disease; ischaemia; neurodegeneration.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200102550-A2.
XX
PD 11-JAN-2001.
XX
PF 03-JUL-2000; 2000WO-BE00077.
XX
PR 01-JUL-1999; 99EP-0870141.
XX
PA (JANC) JANSSEN PHARM NV.
XX
PI Contreras RH, De Backer MD, Luyten WHML, Malcorps IKL;
PI Nellissen BJM, Reekmans RJ;
XX
DR WPI; 2001-367042/38.
DR N-PSDB; AAH29715.
XX
PT Yeast and fungal nucleic acids encoding proteins involved in a pathway
PT leading to programmed cell death, useful for treating proliferative
PT disorders, yeast and fungal infections, or for preventing apoptosis in
PT certain diseases.
XX
PS Claim 1; Fig 1; 218pp; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of apoptosis associated proteins from the yeast Saccharomyces
CC cerevisiae and the fungus Candida albicans. These can be used to identify
CC treatments for fungal and yeast infections, for proliferative diseases
CC and for apoptosis related diseases such as autoimmune diseases, ischaemia
CC and neurodegeneration. The present sequence is one of the S. cerevisiae
CC proteins of the invention.
XX
SQ Sequence 403 AA;

Query Match 3.4%; Score 13; DB 22; Length 403;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 VMACGRPQGTAVY 218
Db 340 vmacgrpqqgtavy 352
|||||

RESULT 20
AAG27202
ID AAG27202 standard; Protein; 133 AA.
XX
AC AAG27202;
XX
DT 17-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 31947.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
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XX termination sequence; corn.
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PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
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PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
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PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
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PR 22-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
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PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 2.9% Score 11; DB 21; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 AGVDGLRVGMG 196
Db 43 agvdglrvgm 53
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RESULT 23
AAG30890
ID AAG30890 standard; Protein; 435 AA.

XX AC AAG30890;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 37008.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
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PR 05-MAY-1999; 99US-0132485.
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PR 08-JUN-1999; 99US-0138094.
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PR 31-AUG-1999; 99US-0151438.
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PR 07-SEP-1999; 99US-0152363.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 2.9%; Score 11; DB 21; Length 435;
Best Local Similarity 100.0%; Pred. No. 0.035; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 186 AGVDGLRVGMG 196
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DB 239 agvdglrvgm 249

RESULT 24
AAG43110
ID AAG43110 standard; Protein; 436 AA.
XX AC AAG43110;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 53844.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
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PR 02-AUG-1999; 99US-0145386.
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PR 09-AUG-1999; 99US-0147493.
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PR 11-AUG-1999; 99US-0148319.
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PR 31-AUG-1999; 99US-0151338.
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PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
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PR 28-OCT-1999; 99US-0161920.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
Query Match 2.9%; Score 11; DB 21; Length 436;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 186 AGVDGLRVGMC 196
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Db 240 agvdglrvgmc 250
RESULT 25
AAG30889
ID AAG30889 standard; Protein; 443 AA.
XX AC AAG30889;
XX AC
XX XX
DT 17-OCT-2000 (first entry)
XX XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37007.
XX XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX XX
OS Arabidopsis thaliana.
XX XX
PN EP1033405-A2.
XX XX
PD 06-SEP-2000.
XX XX
PF 25-FEB-2000; 2000EP-0301439.
XX XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS Arabidopsis thaliana.
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XX PF 25-FEB-2000; 2000EP-0301439.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 2.9% Score 11; DB 21; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 AGVDGLRVGMG 196
Db 306 agvdglrvgm 316
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RESULT 28
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AC AAG43108;
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DT 18-OCT-2000 (first entry)
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XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
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PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR 27-JUL-1999; 99US-0145919.
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PR 23-AUG-1999; 99US-0149930.
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PR 26-AUG-1999; 99US-0150884.
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PR 27-AUG-1999; 99US-0151066.
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PR 30-AUG-1999; 99US-0151303.
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PR 07-SEP-1999; 99US-0152363.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 2.9%; Score 11; DB 21; Length 503;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 307 agvdglrvgm 317

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DT 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

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PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149802.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 13-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.

PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
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PR 14-OCT-1999; 99US-0159331.
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PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160880.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 2.6%; Score 10; DB 21; Length 444;
Best Local Similarity 100.0%; Pred. No. 0.35;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 GVDGLRVGMG 196

Db 249 gvdglrvgm 258

RESULT 31

AAG20989

ID AAG20989 standard; Protein; 503 AA.

XX AAG20989;

AC AAG20989;

XX 17-OCT-2000 (first entry)

DT Arabidopsis thaliana protein fragment SEQ ID NO: 23383.

DE Arabidopsis thaliana

XX

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

PD 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
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PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
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PR 14-MAY-1999; 99US-0134221.
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PR 18-MAY-1999; 99US-0134941.
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PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
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PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
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PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
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PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
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PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
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PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
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PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
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PR 21-JUL-1999; 99US-0145086.
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PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
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PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
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PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
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PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
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PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.

PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
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 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.
 PR 29-OCT-1999; 99US-0162143.

Query Match 2.6%; Score 10; DB 21; Length 503;

Best Local Similarity 100.0%; Pred. No. 0.4;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 GVDGLRVGMG 196

Db 308 GVDGLRVGMG 317

RESULT 32

AAB80108
 ID AAB80108 standard; Protein; 178 AA.

XX AC AAB80108;

XX DT 30-APR-2001 (first entry)

XX DE Corynebacterium glutamicum MP protein sequence SEQ ID NO:950.

XX KW Corynebacterium glutamicum; metabolic pathway protein; MP protein;
 KW fine chemical production; microorganism; organic acid; nucleoside;
 KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;
 KW lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;
 KW carbohydrate; aromatic compound; cofactor; polyketide; enzyme.

XX OS Corynebacterium glutamicum.

XX PN WC200100843-A2.

XX PD 04-JAN-2001.

XX PF 23-JUN-2000; 2000WO-IB00923.

XX PR 25-JUN-1999; 99US-0141031.

PR 01-JUL-1999; 99DE-1030476.

PR 02-JUL-1999; 99US-0142101.

PR 08-JUL-1999; 99DE-1031415.

PR 08-JUL-1999; 99DE-1031418.

PR 08-JUL-1999; 99DE-1031419.

PR 08-JUL-1999; 99DE-1031420.

PR 08-JUL-1999; 99DE-1031424.

PR 08-JUL-1999; 99DE-1031428.

PR 08-JUL-1999; 99DE-1031434.

PR 08-JUL-1999; 99DE-1031435.
 PR 08-JUL-1999; 99DE-1031443.
 PR 08-JUL-1999; 99DE-1031453.
 PR 08-JUL-1999; 99DE-1031457.
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 PR 09-JUL-1999; 99DE-1032206.
 PR 09-JUL-1999; 99DE-1032227.
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 PR 09-JUL-1999; 99DE-1032229.
 PR 09-JUL-1999; 99DE-1032230.
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 PR 14-JUL-1999; 99DE-1033004.
 PR 14-JUL-1999; 99DE-1033005.
 PR 14-JUL-1999; 99DE-1033006.
 PR 12-AUG-1999; 99US-0148613.
 PR 27-AUG-1999; 99DE-1040764.
 PR 27-AUG-1999; 99DE-1040765.
 PR 27-AUG-1999; 99DE-1040766.
 PR 31-AUG-1999; 99DE-1040832.
 PR 31-AUG-1999; 99DE-1041378.
 PR 31-AUG-1999; 99DE-1041379.
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 PR 31-AUG-1999; 99DE-1041394.
 PR 31-AUG-1999; 99DE-1041396.
 PR 03-SEP-1999; 99DE-1042076.
 PR 03-SEP-1999; 99DE-1042077.
 PR 03-SEP-1999; 99DE-1042079.
 PR 03-SEP-1999; 99DE-1042086.
 PR 03-SEP-1999; 99DE-1042087.
 PR 03-SEP-1999; 99DE-1042088.
 PR 03-SEP-1999; 99DE-1042095.
 PR 03-SEP-1999; 99DE-1042124.
 PR 03-SEP-1999; 99DE-1042129.
 PR 09-MAR-2000; 2000US-0187970.

(BADI) BASF AG.

Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;

WPI; 2001-137957/14.

N-PSDB; AAF72227.

Nucleic acids from Corynebacterium glutamicum encoding metabolic
 pathway proteins, useful for producing fine chemicals in
 microorganisms, including organic acids, nonproteinogenic amino acids,
 and purine and pyrimidine bases -

Claim 20; Page 1455; 1737pp; English.

AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic
 pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum
 MP nucleic acids are useful for the production of fine chemicals
 in microorganisms, including organic acids, nonproteinogenic amino
 acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids,
 saturated and unsaturated fatty acids, diols, carbohydrates, aromatic
 compounds, vitamins, cofactors, polyketides and enzymes.

Sequence 178 AA;

Query Match 2.3%; Score 9; DB 22; Length 178;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GVPITADGG 236
Db 16 gvpitadgg 24
|||||

RESULT 33
AAY97820
ID AAY97820 standard; Protein; 489 AA.
XX AC AAY97820;
XX 29-AUG-2000 (first entry)
XX DE Pseudomonas sp. WF505 ORF6-3 protein, SEQ ID NO:5.
XX KW Benzothioophene oxidase; bto gene cluster; desulphurisation; crude oil;
XX KW decontamination.
XX OS Pseudomonas sp. WF505.
XX PN JP2000093180-A.
XX PD 04-APR-2000.
XX PF 28-SEP-1998; 98JP-0272744.
XX PR 28-SEP-1998; 98JP-0272744.
XX PA (TOFU) TONEN CORP.
XX XX
XX WPI; 2000-378972/33.
XX DR N-PSDB; AAA38391.
XX
XX New proteins useful for desulfurization of crude oil have ability to
XX control expression of benzothioophene oxidase group -
XX
XX Example 1; Page 19-20; 43pp; Japanese.
XX
XX The invention relates to proteins encoded by the benzothioophene oxidase
XX (bto) gene cluster from Pseudomonas sp. WF505, specifically the protein
XX which controls expression of the gene cluster (AAY97827), the
XX benzothioophene oxidase (bto) enzyme itself (AAY97825) and a
XX benzothioophene oxidase co-enzyme (AAY97824), which controls
XX benzothioophene activity via redox regulation. These enzymes are
XX respectively encoded by the bto gene cluster open reading frames ORF2-16
XX (AAA38398), ORF4-9 (AAA38396) and ORF6-7 (AAA38395). The invention also
XX encompasses genetic constructs and vectors comprising the genes encoding
XX these proteins, hosts containing such constructs and the recombinant
XX production of the enzymes. Pseudomonas sp. WF505 benzothioophene oxidase,
XX benzothioophene oxidase co-enzyme and bto gene cluster regulator are
XX useful in the desulfurization of crude oil and petroleum products, and
XX for the clarification of soil and waste water contaminated by organic
XX sulphur compounds. Sequences AAY97819-Y97829 represent the proteins
XX encoded by the genes of the Pseudomonas sp. WF505 benzothioophene oxidase
XX gene cluster.
XX
XX Sequence 489 AA;

Query Match 2.3%; Score 9; DB 21; Length 489;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 GASTVMMGS 258
Db 352 gastvmmgs 360
|||||

RESULT 34
AAG90418
ID AAG90418 standard; Protein; 506 AA.
XX AC AAG90418;
XX 26-SEP-2001 (first entry)
XX DE C glutamicum protein fragment SEQ ID NO: 4172.
XX KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
XX KW organic acid synthesis.
XX OS Corynebacterium glutamicum.
XX PN EP1108790-A2.
XX PD 20-JUN-2001.
XX PF 18-DEC-2000; 2000EP-0127688.
XX PR 16-DEC-1999; 99JP-0377484.
XX PR 07-APR-2000; 2000JP-0159162.
XX PR 03-AUG-2000; 2000JP-0280988.
XX PA (KYOW) KYOWA HAKKO KOGYO KK.
XX PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
XX PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX WPI; 2001-376931/40.
XX DR N-PSDB; AAH65637.
XX
XX Novel polynucleotides derived from Coryneform bacteria, for identifying
XX mutation point of a gene, measuring expression of a gene, analysing
XX expression profile or pattern of a gene and identifying homologous gene
XX
XX Claim 17; SEQ ID NO: 4172; 246pp + Sequence Listing; English.
XX
XX The present invention provides a number of nucleotide and protein
XX sequences from the Coryneform bacterium Corynebacterium glutamicum. These
XX are useful for identifying the mutation point of a gene derived from a
XX mutant of coryneform bacterium, measuring expression amount and
XX analysing the expression profile or expression pattern of a gene derived
XX from Coryneform bacterium, and identifying a homologue of a gene derived
XX from coryneform bacterium. Coryneform bacteria are useful for producing
XX amino acids, nucleic acids, vitamins, saccharides and organic acids,
XX particularly L-lysine. The present sequence is a protein described
XX in the exemplification of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from the
XX European Patent Office.
XX
XX Sequence 506 AA;

Query Match 2.3%; Score 9; DB 22; Length 506;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GVPITADGG 236
Db 344 gvpitadgg 352
|||||

RESULT 35
AAB80106
ID AAB80106 standard; Protein; 506 AA.
XX AC AAB80106;
XX 30-APR-2001 (first entry)

XX DE Corynebacterium glutamicum MP protein sequence SEQ ID NO:946.
XX DE
XX DE
KW KW Corynebacterium glutamicum; metabolic pathway protein; MP protein;
KW KW fine chemical production; microorganism; organic acid; nucleoside;
KW KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;
KW KW lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;
KW KW carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
XX OS
XX OS Corynebacterium glutamicum.
XX PN
XX PN WO200100843-A2.
XX PN
XX PN 04-JAN-2001.
XX PF
XX PF 23-JUN-2000; 2000WO-IB00923.
XX PF
XX PF 25-JUN-1999; 99US-0141031.
XX PF 01-JUL-1999; 99DE-1030476.
XX PF 02-JUL-1999; 99US-0142101.
XX PF 08-JUL-1999; 99DE-1031415.
XX PF 08-JUL-1999; 99DE-1031418.
XX PF 08-JUL-1999; 99DE-1031419.
XX PF 08-JUL-1999; 99DE-1031420.
XX PF 08-JUL-1999; 99DE-1031424.
XX PF 08-JUL-1999; 99DE-1031428.
XX PF 08-JUL-1999; 99DE-1031434.
XX PF 08-JUL-1999; 99DE-1031435.
XX PF 08-JUL-1999; 99DE-1031443.
XX PF 08-JUL-1999; 99DE-1031453.
XX PF 08-JUL-1999; 99DE-1031457.
XX PF 08-JUL-1999; 99DE-1031465.
XX PF 08-JUL-1999; 99DE-1031478.
XX PF 08-JUL-1999; 99DE-1031510.
XX PF 08-JUL-1999; 99DE-1031541.
XX PF 08-JUL-1999; 99DE-1031573.
XX PF 08-JUL-1999; 99DE-1031592.
XX PF 08-JUL-1999; 99DE-1031632.
XX PF 08-JUL-1999; 99DE-1031634.
XX PF 08-JUL-1999; 99DE-1031636.
XX PF 08-JUL-1999; 99DE-1032125.
XX PF 08-JUL-1999; 99DE-1032126.
XX PF 08-JUL-1999; 99DE-1032130.
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XX PF 08-JUL-1999; 99DE-1032206.
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XX PF 14-JUL-1999; 99DE-1032922.
XX PF 14-JUL-1999; 99DE-1032926.
XX PF 14-JUL-1999; 99DE-1032928.
XX PF 14-JUL-1999; 99DE-1033004.
XX PF 14-JUL-1999; 99DE-1033005.
XX PF 14-JUL-1999; 99DE-1033006.
XX PF 12-AUG-1999; 99US-0148613.
XX PF 27-AUG-1999; 99DE-1040764.
XX PF 27-AUG-1999; 99DE-1040765.
XX PF 27-AUG-1999; 99DE-1040766.
XX PF 27-AUG-1999; 99DE-1040832.
XX PF 31-AUG-1999; 99DE-1041378.
XX PF 31-AUG-1999; 99DE-1041379.
XX PF 31-AUG-1999; 99DE-1041380.
XX PF 31-AUG-1999; 99DE-1041394.
XX PF 31-AUG-1999; 99DE-1041396.
XX PF 03-SEP-1999; 99DE-1042076.
XX PF 03-SEP-1999; 99DE-1042077.
XX PF 03-SEP-1999; 99DE-1042079.
XX PF 03-SEP-1999; 99DE-1042086.
XX PF 03-SEP-1999; 99DE-1042087.
XX PF 03-SEP-1999; 99DE-1042088.
XX PF 03-SEP-1999; 99DE-1042095.
XX PF 03-SEP-1999; 99DE-1042124.

PR 03-SEP-1999; 99DE-1042129.
PR 09-MAR-2000; 2000US-0187970.
XX
XX (BADI) BASF AG.
XX PA
XX Pompejus M, Kroegeer B, Schroeder H, Zelder O, Haberhauer G;
XX WPI; 2001-137957/14.
DR N-PSDB; AAF72225.
XX
XX Nucleic acids from Corynebacterium glutamicum encoding metabolic
PT pathway proteins, useful for producing fine chemicals in
PT microorganisms, including organic acids, nonproteinogenic amino acids,
PT and purine and pyrimidine bases -
XX
XX Claim 20; Page 1451-1452; 1737pp; English.
XX
XX AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic
CC pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum
CC MP nucleic acids are useful for the production of fine chemicals
CC in microorganisms, including organic acids, nonproteinogenic amino
CC acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids,
CC saturated and unsaturated fatty acids, diols, carbohydrates, aromatic
CC compounds, vitamins, cofactors, polyketides and enzymes.
XX
XX Sequence 506 AA;
SQ
Query Match 2.3%; Score 9; DB 22; Length 506;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 228 GVPPIADGG 236
Db 344 gvpIadgg 352
|||||
RESULT 36
AAR89189
ID AAR89189 standard; peptide; 24 AA.
XX
XX AAR89189;
AC
XX
DT 07-JUN-1996 (first entry)
XX
DE GPR adrenergic receptor TM consensus sequence #10.
XX
XX G-protein coupled receptor; ligand binding assay; transmembrane domain;
KW psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin;
KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
KW rhodopsin; opsin; odorant; cytomegalovirus; serotonergic.
XX
XX Synthetic.
XX
XX WO9405695-A1.
PN
XX
PD 17-MAR-1994.
XX
XX
PF 09-SEP-1993; 93WO-US08528.
XX
PR 10-SEP-1992; 92US-0943236.
XX
XX (UYN) UNIV NEW YORK STATE.
PA
XX Murphy RB, Schuster DI;
PI
XX WPI; 1994-101120/12.
DR
XX Polypeptides of G-coupled receptor proteins (GPRs) - useful for
PT binding GPR ligands or modulating GPR binding
XX
XX Claim 8; Page 136; 160pp; English.
XX

CC The sequence of a polypeptide, based on the consensus sequence from
 CC transmembrane domains of adrenergic receptors, used in a G-protein
 CC coupled receptor ligand binding assay. The assay can be used to
 CC identify fragments pref. transmembrane fragments, from G-protein coupled
 CC receptor (GPR) proteins (see AAR48686-R48758 for examples) which retain
 CC biological activity such as binding a GPR ligand or modulating GPR ligand
 CC binding to a GPR (see AAR48759-R48758, AAR50569-R50807 and
 CC AAR89189-R89195 for examples of polypeptide fragments). The polypeptide
 CC fragments can be used in compositions for treating subjects suffering
 CC from a pathology related to a GPR abnormality e.g. a psychotic disorder
 CC such as schizophrenia.
 XX

XX Sequence 24 AA;

Query Match 2.1%; Score 8; DB 15; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 IGGNVVTA 177
 Db 15 iggnvvta 22
 |||||

RESULT 37

AAR50808
 ID AAR50808 standard; peptide; 24 AA.

XX AAR50808;

DT 17-MAY-1996 (first entry)

DE G-protein coupled serotonergic receptor consensus sequence #4.

KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin;
 KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
 KW rhodopsin; opsin; odorant; cytomegalovirus; serotonergic.

XX Synthetic.

XX WO9405695-A1.

XX 17-MAR-1994.

XX 09-SEP-1993; 93WO-US08528.

XX 10-SEP-1992; 92US-0943236.

XX (UUNY) UNIV NEW YORK STATE.

XX Murphy RB, Schuster DI;

XX WPI; 1994-101120/12.

XX Polypeptides of G-coupled receptor proteins (GPRs) - useful for
 PT binding GPR ligands or modulating GPR binding

XX Disclosure; Page 34; 160pp; English.

XX Peptides AAR50808-14 are peptides based on serotonergic receptor (5-HT)
 CC transmembrane domain consensus sequences, used in a G-protein coupled
 CC receptor ligand binding assay. The assay can be used to identify
 CC fragments pref. transmembrane fragments, from G-protein coupled receptor
 CC (GPR) proteins (see AAR48686-R48758 for examples) which retain
 CC biological activity such as binding a GPR ligand or modulating GPR ligand
 CC binding to a GPR (see AAR48759-R48758, AAR50569-R50807 and
 CC AAR89189-R89195 for examples of polypeptide fragments). The polypeptide
 CC fragments can be used in compositions for treating subjects suffering
 CC from a pathology related to a GPR abnormality e.g. a psychotic disorder
 CC such as schizophrenia.
 XX

XX Sequence 24 AA;

Query Match 2.1%; Score 8; DB 15; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 IGGNVVTA 177
 Db 15 iggnvvta 22
 |||||

RESULT 38

AAW02740
 ID AAW02740 standard; peptide; 24 AA.

XX AAW02740;

DT 13-NOV-1996 (first entry)

DE G-protein coupled serotonergic (5-HT) receptor consensus sequence #4.

KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;
 KW muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
 KW odorant; cytomegalovirus; serotonergic.

XX Synthetic.

XX US5508384-A.

XX 16-APR-1996.

XX 10-SEP-1992; 92US-0943236.

XX 09-SEP-1993; 93US-0118270.

XX 10-SEP-1992; 92US-0943236.

XX (UUNY) UNIV NEW YORK STATE.

XX Murphy RB, Schuster DI;

XX WPI; 1996-208785/21.

XX New dopamine receptor peptide - useful as antipsychotic agent, e.g.
 PT for treating schizophrenia

XX Disclosure; Column 27; 184pp; English.

XX The sequence of a polypeptide, based on the serotonergic receptor (5-HT)
 CC transmembrane domain consensus sequences, used in a G-protein coupled
 CC receptor ligand binding assay. The assay can be used to identify
 CC fragments pref. transmembrane fragments, from G-protein coupled receptor
 CC (GPR) proteins (AAW02657-W02730) which retain biological activity such
 CC as binding a GPR ligand or modulating GPR ligand binding to a GPR (see
 CC AAW02747-W02999 for examples of polypeptide fragments). The polypeptide
 CC fragments can be used in compositions for treating subjects suffering
 CC from a pathology related to a GPR abnormality e.g. a psychotic disorder
 CC such as schizophrenia.
 XX

XX Sequence 24 AA;

Query Match 2.1%; Score 8; DB 17; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 IGGNVVTA 177
 Db 15 iggnvvta 22
 |||||

RESULT 39

AAV35259

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ID AAY35259 standard; Protein; 86 AA.
XX
AC AAY35259;
XX
XX
DT 13-SEP-1999 (first entry)
XX
XX Chlamydia pneumoniae ribosomal polypeptide.
XX
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW vaccine; neutralising epitope.
XX
XX Chlamydia pneumoniae.
OS
XX WO9927105-A2.
PN
XX 03-JUN-1999.
PD
XX 20-NOV-1998; 98WO-IB01890.
PF
XX 04-NOV-1998; 98US-0107078.
PR
XX 21-NOV-1997; 97FR-0014673.
XX
PA (GEST ) GENSET.
XX
XX Griffais R;
PI
XX WPI; 1999-357842/30.
DR
XX
XX Genome sequence of Chlamydia pneumoniae
PT
XX Page 1092-1093; Disclosure; 1912pp; English.
PS
XX AAY34584-Y35879 represent the proteins encoded by all the open reading
CC frames in the complete genome (see AAX91950) of Chlamydia pneumoniae.
CC C. pneumoniae causes respiratory disease such as pneumonia and
CC bronchitis and is thought to be a contributing factor in heart
CC disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in
CC immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotide sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae.
XX
SQ Sequence 86 AA;

Query Match 2.1%; Score 8; DB 20; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 SEGDKVKI 309
Db 57 segdkvki 64
|||||||

RESULT 40
AAG51650
ID AAG51650 standard; Protein; 139 AA.
XX
AC AAG51650;
XX
XX 18-OCT-2000 (first entry)
DT
XX Arabidopsis thaliana protein fragment SEQ ID NO: 65575.
DE
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
OS
XX
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PN EP1033405-A2.
XX
XX 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
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PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
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PR 29-OCT-1999; 99US-0162142.

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Best Local Similarity 100.0%; Pred. No. 12;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 DGLTAQQL 23
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Db 120 dgltaqql 127

Search completed: September 26, 2002, 08:32:00
Job time: 259 sec

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OM protein - protein search, using sw model

Run on: September 26, 2002, 08:28:21 ; Search time 13.07 Seconds
(without alignments)
717.630 Million cell updates/sec

Title: US-09-853-918-30
Perfect score: 384
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

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Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Issued_Patents_AA.*

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SUMMARIES

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5	8	2.1	158	3	US-09-053-197A-19
6	8	2.1	158	4	US-09-085-761A-19
7	7	1.8	32	3	US-09-082-090-5
8	7	1.8	369	1	US-08-253-823-1
9	7	1.8	369	1	US-08-290-508-3
10	7	1.8	369	2	US-08-606-144-1
11	7	1.8	369	5	PCT-US94-02174-3
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24	6	1.6	23	2	US-08-856-034-14
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27	6	1.6	24	1	US-08-628-291-14
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34	6	1.6	66	2	US-08-511-485-25
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38	6	1.6	72	3	US-08-473-034-7
39	6	1.6	73	1	US-08-355-888A-11
40	6	1.6	73	2	US-08-693-697-11
41	6	1.6	73	3	US-08-693-696-11
42	6	1.6	80	4	US-08-858-207A-530
43	6	1.6	84	4	US-09-247-155-173
44	6	1.6	92	2	US-09-047-125-13
45	6	1.6	92	3	US-07-736-335E-13
46	6	1.6	94	2	US-08-828-008-2
47	6	1.6	95	1	US-08-202-389-21
48	6	1.6	95	1	US-08-202-389-22
49	6	1.6	95	1	US-08-202-389-23
50	6	1.6	107	6	5242821-8
51	6	1.6	113	4	US-08-836-075A-62
52	6	1.6	117	4	US-09-227-357-269
53	6	1.6	129	4	US-09-107-383-13
54	6	1.6	171	1	US-08-118-469A-2
55	6	1.6	171	1	US-08-909-119-2
56	6	1.6	176	1	US-08-036-210-9
57	6	1.6	176	2	US-08-449-609-9
58	6	1.6	177	5	PCT-US96-03916-19
59	6	1.6	178	2	US-08-487-031-23
60	6	1.6	178	3	US-08-473-034-23
61	6	1.6	223	4	US-09-377-557-16
62	6	1.6	233	1	US-07-890-422B-1
63	6	1.6	244	4	US-09-371-710-31
64	6	1.6	244	4	US-09-648-386-31
65	6	1.6	245	2	US-08-685-992-26
66	6	1.6	245	2	US-09-144-925-26
67	6	1.6	246	4	US-09-627-376-15
68	6	1.6	252	2	US-08-853-659A-43
69	6	1.6	253	1	US-08-399-696-4
70	6	1.6	253	1	US-08-399-696-118
71	6	1.6	256	2	US-08-578-516-6
72	6	1.6	259	3	US-09-082-090-2
73	6	1.6	263	1	US-07-901-707-4
74	6	1.6	263	1	US-07-988-430-4
75	6	1.6	263	1	US-08-423-336-4
76	6	1.6	263	1	US-08-488-113B-4
77	6	1.6	263	1	US-08-477-484B-4
78	6	1.6	263	2	US-08-646-360-4
79	6	1.6	263	4	US-08-839-765-4
80	6	1.6	263	4	US-09-136-389-4
81	6	1.6	263	5	PCT-US92-09487-4
82	6	1.6	271	2	US-08-467-265-2
83	6	1.6	271	4	US-08-467-265-2
84	6	1.6	271	4	US-09-407-891-2
85	6	1.6	279	4	US-09-330-970-5
86	6	1.6	281	4	US-08-961-083-196
87	6	1.6	286	1	US-08-324-301-13
88	6	1.6	305	2	US-08-853-659A-47
89	6	1.6	311	2	US-08-568-459A-21
90	6	1.6	311	2	US-08-487-826B-33
91	6	1.6	312	3	US-09-154-874-6
92	6	1.6	318	1	US-08-628-291-16
93	6	1.6	318	2	US-09-128-722-16
94	6	1.6	318	3	US-09-120-365-77
95	6	1.6	318	4	US-09-515-039-77
96	6	1.6	322	1	US-08-036-210-11
97	6	1.6	322	2	US-08-449-609-11
98	6	1.6	326	2	US-08-997-080-43
99	6	1.6	326	2	US-08-997-362-43
100	6	1.6	326	3	US-08-873-970-43

ALIGNMENTS

```
RESULT 1
US-08-925-230-7
; Sequence 7, Application US/08925230
; Patent No. 6147194
; GENERAL INFORMATION:
; APPLICANT: Collart, Frank
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO IMPDH
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,230
; FILING DATE: September 8, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 5,665,583
; FILING DATE: 12-AUG-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:274
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-925-230-7

Query Match      8.1%; Score 31; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.9e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGASTVMGSLLAATTEAPGEYFFSDG 275
DB 375 KALALGASTVMGSLLAATTEAPGEYFFSDG 405
|||||
RESULT 2
US-08-925-230-8
; Sequence 8, Application US/08925230
; Patent No. 6147194
; GENERAL INFORMATION:
; APPLICANT: Collart, Frank
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO IMPDH
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,230
; FILING DATE: September 8, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 5,665,583
; FILING DATE: 12-AUG-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:274
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-925-230-8

Query Match      8.1%; Score 31; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.9e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGASTVMGSLLAATTEAPGEYFFSDG 275
DB 375 KALALGASTVMGSLLAATTEAPGEYFFSDG 405
|||||
```

```
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,230
FILING DATE: September 8, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 5,665,583
FILING DATE: 12-AUG-1988
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:274
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-925-230-8

Query Match      8.1%; Score 31; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.9e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGASTVMGSLLAATTEAPGEYFFSDG 275
DB 375 KALALGASTVMGSLLAATTEAPGEYFFSDG 405
|||||
RESULT 3
US-08-118-270-89
; Sequence 89, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2A
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-89

Query Match 2.1%; Score 8; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 IGGNVVTA 177
Db 15 IGGNVVTA 22
|||||

RESULT 4

PCT-US93-08528-89
Sequence 89, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633

INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-89

Query Match 2.1%; Score 8; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 IGGNVVTA 177
Db 15 IGGNVVTA 22
|||||

RESULT 5

US-09-053-197A-19
Sequence 19, Application US/09053197A
Patent No. 6022952
GENERAL INFORMATION:
APPLICANT: Weiner, Joel H.
APPLICANT: Turner, Raymond J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTEIN
TITLE OF INVENTION: SECRETION
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,197A
FILING DATE: 01-APR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UALB-03293
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-053-197A-19

Query Match 2.1%; Score 8; DB 3; Length 158;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 APGEYFFS 273
Db 49 APGEYFFS 56
|||||

RESULT 6

US-09-085-761A-19
Sequence 19, Application US/09085761A
Patent No. 6335178
GENERAL INFORMATION:
APPLICANT: Weiner, Joel H.
APPLICANT: Turner, Raymond J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTEIN
TITLE OF INVENTION: SECRETION
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,761A
; FILING DATE: 28-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Carroll, Peter G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: UALB-03356
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-085-761A-19

Query Match 2.1%; Score 8; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 APGEYFFS 273
Db 49 APGEYFFS 56

RESULT 7
US-09-082-090-5
; Sequence 5, Application US/09082090
; Patent No. 6090583
; GENERAL INFORMATION:
; APPLICANT: CLINKENBEARD, HELEN
; APPLICANT: SOUTHAN, CHRISTOPHER
; APPLICANT: BURGESS, NICOLA
; TITLE OF INVENTION: No. 6090583el compounds
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,090
; FILING DATE: 20-MAY-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711310.4
; FILING DATE: 30-MAY-1997
; APPLICATION NUMBER: GB 9803690.8
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F.
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-30332
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-082-090-5

Query Match 1.8%; Score 7; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 SLSVLRS 351
Db 17 SLSVLRS 23

RESULT 8
US-08-253-823-1
; Sequence 1, Application US/08253823
; Patent No. 5541094
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: GLYCOLATE OXIDASE PRODUCTION
; NUMBER OF SEQUENCES: 1
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM
; OPERATING SYSTEM: MICROSOFT WINDOWS V3.0
; SOFTWARE: MICROSOFT WORD V2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,823
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/085,488
; FILING DATE: JULY 1, 1993
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-253-823-1

Query Match 1.8%; Score 7; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGA 251
Db 296 KALALGA 302

RESULT 9
US-08-290-508-3
; Sequence 3, Application US/08290508
; Patent No. 5693490
; GENERAL INFORMATION:
; APPLICANT: PAYNE, MARK S.
; APPLICANT: ANTON, DAVID L.
; APPLICANT: DICOSIMO, ROBERT
; APPLICANT: GAVAGAN, JOHN E.
; TITLE OF INVENTION: Production of glycolate oxidase
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE

COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH 1.0 MB
COMPUTER: MACINTOSH
OPERATING SYSTEM: MACINTOSH SYSTEM, 6.0
SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290.508
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/025.495
FILING DATE: 03-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: GALLEGO, R. THOMAS
REGISTRATION NUMBER: 32.692
REFERENCE/DOCKET NUMBER: CR-9271
TELEPHONE: 302-892-7342
TELEFAX: 302-892-7949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-290-508-3

Query Match 1.8%; Score 7; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGA 251
Db 296 KALALGA 302

RESULT 10
US-08-606-144-1
Sequence 1, Application US/08606144
Patent No. 5834262
GENERAL INFORMATION:
APPLICANT: DAVID LEROY ANTON
APPLICANT: ROBERT DICOSIMO
TITLE OF INVENTION: OXIDATION OF GLYCOLIC ACID TO
TITLE OF INVENTION: GLYOXILIC ACID USING A
TITLE OF INVENTION: MICROBIAL CELL TRANSFORMANT
TITLE OF INVENTION: AS CATALYST
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.JI.DJUIPONTJDEINEMOURS
ADDRESSEE: AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH 2.0 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS, 3.1
SOFTWARE: MICROSOFT WORD VERSION 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606.144
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/817.165
FILING DATE: JANUARY 6, 1992
ATTORNEY/AGENT INFORMATION:

NAME: GREGORY, THEODORE C.
REGISTRATION NUMBER: 25,243
REFERENCE/DOCKET NUMBER: CH-2087-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4925
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-606-144-1

Query Match 1.8%; Score 7; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGA 251
Db 296 KALALGA 302

RESULT 11
PCT-US94-02174-3
Sequence 3, Application PC/TUS9402174
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Production of
TITLE OF INVENTION: glycolate oxidase IN
TITLE OF INVENTION: methylotrophic yeast
NUMBER OF SEQUENCES: 3
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH 1.0 MB
COMPUTER: MACINTOSH
OPERATING SYSTEM: MACINTOSH SYSTEM, 6.0
SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02174
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US94-02174-3

Query Match 1.8%; Score 7; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGA 251
Db 296 KALALGA 302

RESULT 12
US-08-191-866D-21
Sequence 21, Application US/08191866D
Patent No. 5783195
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
APPLICANT: Macdonald, Richard D.
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Rhinotracheitis Virus S-IBR-052 And Uses Thereof
NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/191,866D
FILING DATE: 4 February 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-191-866D-21

Query Match 1.8%; Score 7; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 LLCGAAV 120
Db 16 LLCGAAV 22

RESULT 13
US-08-185-949B-21
Sequence 21, Application US/08185949B
Patent No. 5874279
GENERAL INFORMATION:
APPLICANT: Mark D. Cochran
APPLICANT: Richard D. Macdonald
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Rhinotracheitis Virus
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,949B
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: ,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 278-0525
INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-185-949B-21

Query Match 1.8%; Score 7; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 LLCGAAV 120
Db 16 LLCGAAV 22

RESULT 14
US-08-843-417-10
Sequence 10, Application US/08843417
Patent No. 6184349
GENERAL INFORMATION:
APPLICANT: Herman, Ronald C
APPLICANT: Delgado, Stephen G
APPLICANT: Fish, Linda M
APPLICANT: Sangameswaran, Lakshmi
APPLICANT: Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 525 University Ave
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.A.
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,417
FILING DATE: April 15, 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28340-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)-324-7041
TELEFAX: (415)-324-0638
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-843-417-10

Query Match 1.8%; Score 7; DB 4; Length 1956;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 SLSVLRS 351
Db 751 SLSVLRS 757

RESULT 15
US-09-036-987A-6
; Sequence 6, Application US/09036987A
; Patent No. 6143526
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H.
; APPLICANT: Broughton, Mary C.
; APPLICANT: Crawford, Kathryn P.
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Merlo, Donald J.
; APPLICANT: Treadway, Patti J.
; APPLICANT: Turner, Jan R.
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; TITLE OF INVENTION: Production
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow Agrosciences LLC Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,987A
; FILING DATE: 09-MAR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R.
; REGISTRATION NUMBER: 28,479
; REFERENCE/DOCKET NUMBER: 50,608
; TELEPHONE: (317)337-4816
; TELEFAX: (317)337-4847
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5588 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-036-987A-6

Query Match 1.8%; Score 7; DB 4; Length 5588;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LISGGTG 11
Db 1407 LISGGTG 1413

RESULT 16
US-09-370-700-6
; Sequence 6, Application US/09370700
; Patent No. 6274350
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H.
; APPLICANT: Broughton, Mary C.
; APPLICANT: Crawford, Kathryn P.
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Treadway, Patti J.
; APPLICANT: Turner, Jan R.
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; FILE REFERENCE: 50489 DIV1
; CURRENT APPLICATION NUMBER: US/09/370,700

; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/36987
; EARLIER FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 5588
; TYPE: PRT
; ORGANISM: Saccharopolyspora spinosa
US-09-370-700-6

Query Match 1.8%; Score 7; DB 4; Length 5588;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LISGGTG 11
Db 1407 LISGGTG 1413

RESULT 17
US-08-484-044-8
; Sequence 8, Application US/08484044
; Patent No. 5552282
; GENERAL INFORMATION:
; APPLICANT: Caskey, C. T.
; APPLICANT: Fu, Ying-Hui
; APPLICANT: Friedman, David L.
; APPLICANT: Pizzuti, Antonio
; APPLICANT: Fenwick, Raymond G.
; TITLE OF INVENTION: Diagnosis of Myotonic Muscular Dystrophy
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,044
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/019,940
; FILING DATE: 19-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5443
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-044-8

Query Match 1.6%; Score 6; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EDGLTA 20
|||||
Db 3 EDGLTA 8

RESULT 18

US-09-140-149-11
; Sequence 11, Application US/09140149
; Patent No. 6117680
; APPLICANT: Natesan, Sridaran
; APPLICANT: Gilman, Michael Z
; TITLE OF INVENTION: No. 6117680el Compositions and Methods for Regulation of
; FILE REFERENCE: Transcription
; FILE REFERENCE: 363C
; CURRENT APPLICATION NUMBER: US/09/140,149
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 08/918,401
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: 08/920,610
; EARLIER FILING DATE: 1997-08-27
; EARLIER APPLICATION NUMBER: 09/126,009
; EARLIER FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: PC1/US97/15219
; EARLIER FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-09-140-149-11

Query Match 1.6%; Score 6; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 ALALGA 251
|||||
Db 2 ALALGA 7

RESULT 19

US-08-399-696-109
; Sequence 109, Application US/08399696
; Patent No. 5756669
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: p53-BINDING POLYPEPTIDES AND
; POLYNUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 126
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,696
; FILING DATE: 02-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/156,671
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15522-000710
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-399-696-109

Query Match 1.6%; Score 6; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 AQAKNL 183
|||||
Db 1 AQAKNL 6

RESULT 20

US-08-112-208C-14
; Sequence 14, Application US/08112208C
; Patent No. 5691179
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/112,208C
; FILING DATE: 26-AUG-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-112-208C-14

Query Match 1.6%; Score 6; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 FFSDGV 276
|||||
Db 4 FFSDGV 9

RESULT 21

US-08-248-819A-16

; Sequence 16, Application US/08248819A
; Patent No. 5700638
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248.819A
; FILING DATE: 25-NAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112.208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-248-819A-16

Query Match 1.6%; Score 6; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

Qy 271 FFSDGV 276
Db 4 FFSDGV 9

RESULT 22
US-08-337-646A-34
; Sequence 34, Application US/08337646A
; Patent No. 5856171
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337.646A

; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248.819
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112.208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-337-646A-34

Query Match 1.6%; Score 6; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

Qy 271 FFSDGV 276
Db 4 FFSDGV 9

RESULT 23
US-08-856-531-14
; Sequence 14, Application US/08856531
; Patent No. 5942490
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howell & Haferkamp, L.C.
; STREET: 7733 Forsyth Blvd., Suite 1400
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856.531
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, Donald R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 976176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:

; NAME/KEY: Peptide
; LOCATION: 1..23
; OTHER INFORMATION: /note= "Peptide fragment from
; OTHER INFORMATION: Figure 14A"
US-08-856-531-14

Query Match 1.6%; Score 6; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 FFSDGV 276
Db 4 FFSDGV 9

RESULT 24
US-08-856-034-14
; Sequence 14, Application US/08856034
; Patent No. 5955595
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howell & Haferkamp, L.C.
; STREET: 7733 Forsyth Blvd., Suite 1400
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63105

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,034
; FILING DATE:

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, Donald R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 976175
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092

; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:

; NAME/KEY: Peptide
; LOCATION: 1..23
; OTHER INFORMATION: /note= "Peptide fragment from
; OTHER INFORMATION: Figure 14A"
US-08-856-034-14

Query Match 1.6%; Score 6; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 FFSDGV 276
Db 4 FFSDGV 9

RESULT 25
US-08-808-277A-16

; Sequence 16, Application US/08808277A
; Patent No. 5998374
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: LEE, IN-HEE
; APPLICANT: ZHAO, CHENGQUAN
; TITLE OF INVENTION: CLAVASPIRINS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,277A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 220002057300
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:

; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5998374e
US-08-808-277A-16

Query Match 1.6%; Score 6; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 240 VGHVVK 245
Db 12 VGHVVK 17

RESULT 26
US-08-927-326-34
; Sequence 34, Application US/08927326
; Patent No. 6184202
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/927,326
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/337,646
;; FILING DATE: 10-NOV-1994
;; APPLICATION NUMBER: US 08/248,819
;; FILING DATE: 25-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/112,208
;; FILING DATE: 26-AUG-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 15726A-000620
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 34:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 23 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
US-08-927-326-34

Query Match 1.6%; Score 6; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 FFSQGV 276
Db 4 FFSQGV 9

RESULT 27
US-08-628-291-14
;; Sequence 14, Application US/08628291
;; Patent No. 5801031
;; GENERAL INFORMATION:
;; APPLICANT: GALIVAN, JOHN H.
;; APPLICANT: RYAN, THOMAS J.
;; APPLICANT: YAO, RONG
;; APPLICANT: NIMEC, ZENIA
;; TITLE OF INVENTION: GAMMA GLUTAMYL HYDROLASE
;; NUMBER OF SEQUENCES: 16
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
;; COUNTRY: USA
;; ZIP: 14603
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/628,291
;; FILING DATE:
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: TIMIAN, SUSAN J.
;; REGISTRATION NUMBER: 34,103
;; REFERENCE/DOCKET NUMBER: 20894/150
;; TELEPHONE: 716-263-1636
;; TELEFAX: 716-263-1600
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 24 amino acids

;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-628-291-14

Query Match 1.6%; Score 6; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 LLCGAA 119
Db 14 LLCGAA 19

RESULT 28
US-09-128-722-14
;; Sequence 14, Application US/09128722
;; Patent No. 5962235
;; GENERAL INFORMATION:
;; APPLICANT: Galivan, John H
;; APPLICANT: Ryan, Thomas J
;; APPLICANT: Yao, Rong
;; APPLICANT: Nimec, Zenia
;; TITLE OF INVENTION: Gamma Glutamyl Hydrolase
;; NUMBER OF SEQUENCES: 16
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Jaeckie Fleischmann & Mugel, LLP
;; STREET: 39 State Street
;; CITY: Rochester
;; STATE: New York
;; COUNTRY: US
;; ZIP: 14614-1310
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/128,722
;; FILING DATE: 04-AUG-1998
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/628,291
;; FILING DATE: 05-APR-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Braham, Susan J
;; REGISTRATION NUMBER: 34,103
;; REFERENCE/DOCKET NUMBER: 87681.98R196
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 716-262-3640
;; TELEFAX: 716-262-4133
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 24 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-128-722-14

Query Match 1.6%; Score 6; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 LLCGAA 119
Db 14 LLCGAA 19

RESULT 29

```

RESULT 30
US-08-975-080-29
; Sequence 29, Application US/08975080
; Patent No. 6245523
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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1  RESULT 31
2  US-08-975-080-32
3  ; Sequence 32, Application US/08975080
4  ; Patent No. 6245523
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Altieri, Dario C.
7  ; TITLE OF INVENTION: SURVIVAL, A PROTEIN THAT INHIBITS
8  ; TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
9  ; NUMBER OF SEQUENCES: 35
10 ; CORRESPONDENCE ADDRESS:
11 ; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
12 ; STREET: 1800 M Street, N.W.
13 ; CITY: Washington
14 ; STATE: D.C.
15 ; COUNTRY: USA
16 ; ZIP: 20036-5869
17 ; COMPUTER READABLE FORM:
18 ; MEDIUM TYPE: Floppy disk
19 ; COMPUTER: IBM PC compatible
20 ; OPERATING SYSTEM: PC-DOS/MS-DOS
21 ; SOFTWARE: Patentin Release #1.0, Version #1.30
22 ; CURRENT APPLICATION DATA:
23 ; APPLICATION NUMBER: US/08/975,080
24 ; FILING DATE: 20-NOV-1997
25 ; PRIOR APPLICATION DATA:
26 ; APPLICATION NUMBER: US 60/031,435
27 ; FILING DATE: 20-NOV-1996
28 ; ATTORNEY/AGENT INFORMATION:
29 ; NAME: Adler, Reid G.
30 ; REGISTRATION NUMBER: 30,988
31 ; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
32 ; TELECOMMUNICATION INFORMATION:
33 ; TELEPHONE: 202-467-7000
34 ; TELEFAX: 202-467-7176
35 ; INFORMATION FOR SEQ ID NO: 32:
36 ; SEQUENCE CHARACTERISTICS:
37 ; LENGTH: 50 amino acids
38 ; TYPE: amino acid
39 ; STRANDEDNESS:
40 ; TOPOLOGY: linear
41 ; MOLECULE TYPE: protein

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US-08-975-080-32

Query Match 1.6%; Score 6; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 303 EGDVK 308
DB 4 EGDVK 9

RESULT 32

US-08-630-916A-82
; Sequence 82, Application US/08630916A
; Patent No. 601137
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; APPLICANT: Kay, Brian K.
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,916A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-916A-82

Query Match 1.6%; Score 6; DB 3; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 15 EDGLTA 20
DB 8 EDGLTA 13

RESULT 33

US-08-511-485-24
; Sequence 24, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen

; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
US-08-511-485-24

Query Match 1.6%; Score 6; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 303 EGDVK 308
DB 30 EGDVK 35

RESULT 34

US-08-511-485-25
; Sequence 25, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
; US-08-511-485-25

Query Match 1.6%; Score 6; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 EGDVKV 308
Db 30 EGDVKV 35

RESULT 35
US-08-487-031-17
; Sequence 17, Application US/08487031
; Patent No. 5977306
; GENERAL INFORMATION:
; APPLICANT: Grieve, Robert B.
; APPLICANT: Frank, Glenn R.
; APPLICANT: Mika-Grieve, Marcia
; APPLICANT: Tripp, Cynthia A.
; TITLE OF INVENTION: NOVEL PARASITIC HELMINTH P39
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,031
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: 2618-34-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-487-031-17

Query Match 1.6%; Score 6; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 GELKFE 361
Db 59 GELKFE 64

RESULT 36
US-08-473-034-17
; Sequence 17, Application US/08473034
; Patent No. 6114142
; GENERAL INFORMATION:
; APPLICANT: Grieve, Robert B.
; APPLICANT: Frank, Glenn R.
; APPLICANT: Mika-Grieve, Marcia
; APPLICANT: Tripp, Cynthia A.
; TITLE OF INVENTION: NOVEL PARASITIC HELMINTH P39
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,034
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: 2618-34
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-473-034-17

Query Match 1.6%; Score 6; DB 3; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 GELKFE 361
Db 59 GELKFE 64

RESULT 37
US-08-487-031-7
; Sequence 7, Application US/08487031
; Patent No. 5977306
; GENERAL INFORMATION:
; APPLICANT: Grieve, Robert B.
; APPLICANT: Frank, Glenn R.
; APPLICANT: Mika-Grieve, Marcia
; APPLICANT: Tripp, Cynthia A.
; TITLE OF INVENTION: NOVEL PARASITIC HELMINTH P39
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; US-08-487-031-7

Query Match 1.6%; Score 6; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 GELKFE 361
Db 59 GELKFE 64

RESULT 37
US-08-487-031-7
; Sequence 7, Application US/08487031
; Patent No. 5977306
; GENERAL INFORMATION:
; APPLICANT: Grieve, Robert B.
; APPLICANT: Frank, Glenn R.
; APPLICANT: Mika-Grieve, Marcia
; APPLICANT: Tripp, Cynthia A.
; TITLE OF INVENTION: NOVEL PARASITIC HELMINTH P39
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; US-08-487-031-7
```

ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,031
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2618-34-1
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-031-7

Query Match 1.6%; Score 6; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 356 GELKFE 361
Db 59 GELKFE 64

RESULT 38
US-08-473-034-7
Sequence 7, Application US/08473034
Patent No. 6114142
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Frank, Glenn R.
APPLICANT: Mika-Grieve, Marcia
APPLICANT: Tripp, Cynthia A.
TITLE OF INVENTION: NOVEL PARASITIC HELMINTH P39
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,034
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2618-34
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-473-034-7

Query Match 1.6%; Score 6; DB 3; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 356 GELKFE 361
Db 59 GELKFE 64

RESULT 39
US-08-355-888A-11
Sequence 11, Application US/08355888A
Patent No. 5763211
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: HU-BI.219, A NOVEL HUMAN HEMATOPOIETIN
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/355,888A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-355-888A-11

Query Match 1.6%; Score 6; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 209 CGRPQG 214
Db 31 CGRPQG 36

RESULT 40
US-08-693-697-11
; Sequence 11, Application US/08693697
; Patent No. 5869610
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,697
; FILING DATE: 05-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0037-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-693-697-11

Query Match 1.6%; Score 6; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 CGRPQG 214
|
Db 31 CGRPQG 36

Search completed: September 26, 2002, 08:32:21
Job time: 240 sec

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OM protein - protein search, using sw model

Run on: September 26, 2002, 08:29:26 ; Search time 20.9 seconds
(without alignments)
1765.469 Million cell updates/sec

Title: US-09-853-918-30

Perfect score: 384

Sequence: 1 MADYLISGCTGVVPEDGLTA.....MSAQIEGCVHGLHSYEKRLY 384

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : PIR_71.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	271	70.6	514	1 A35566	IMP dehydrogenase
2	31	8.1	514	1 A31997	IMP dehydrogenase
3	31	8.1	514	1 B31997	IMP dehydrogenase
4	31	8.1	514	1 J70565	IMP dehydrogenase
5	23	6.0	537	1 S41064	IMP dehydrogenase
6	23	6.0	537	1 S59508	IMP dehydrogenase
7	21	5.5	523	1 S59402	IMP dehydrogenase
8	21	5.5	523	1 S48997	IMP dehydrogenase
9	21	5.5	524	1 S50890	IMP dehydrogenase
10	14	3.6	509	2 J7305	IMP dehydrogenase
11	14	3.6	514	1 A38668	IMP dehydrogenase
12	13	3.4	403	1 S53477	IMP dehydrogenase
13	13	3.4	499	1 T32709	IMP dehydrogenase
14	13	3.4	524	1 T40127	IMP dehydrogenase
15	11	2.9	502	2 F86298	IMP dehydrogenase
16	11	2.9	503	1 J64999	IMP dehydrogenase
17	10	2.6	485	2 D83652	inositol-monophosph
18	10	2.6	485	2 D97232	IMP dehydrogenase
19	10	2.6	742	2 H95270	probable kinase/es
20	9	2.3	444	1 D72631	probable IMP dehyd
21	9	2.3	482	2 C72264	IMP dehydrogenase
22	9	2.3	495	2 S34810	probable oxygenase
23	9	2.3	496	1 G54501	IMP dehydrogenase
24	9	2.3	512	1 A55407	IMP dehydrogenase
25	9	2.3	1035	1 GNFFG1	retrovirus-related
26	8	2.1	86	2 H72054	ribosomal protein
27	8	2.1	86	2 C86570	S17 ribosomal prot
28	8	2.1	157	1 S78078	IMP dehydrogenase-
29	8	2.1	206	2 AE0160	probable glutathio

30	2.1	208	2	C96948	deoxyphosphoglucon
31	2.1	254	2	S73185	hypothetical prote
32	2.1	283	2	T09388	(S)-2-hydroxy-acid
33	2.1	290	2	T07032	(S)-2-hydroxy-acid
34	2.1	302	2	H96792	unknown protein F1
35	2.1	325	1	A71887	probable GMP reduc
36	2.1	326	1	C70015	probable GMP reduc
37	2.1	327	1	F64626	probable GMP reduc
38	2.1	327	2	D97326	GMP reductase [imp
39	2.1	328	2	A95145	conserved hypothet
40	2.1	328	2	G98012	GMP reductase [imp
41	2.1	358	2	AC1610	hypothetical prote
42	2.1	364	2	C84221	hypothetical prote
43	2.1	367	2	T10242	(S)-2-hydroxy-acid
44	2.1	368	2	T04532	probable (S)-2-hyd
45	2.1	368	2	G85206	glycolate oxidase-
46	2.1	368	2	A71727	hypothetical prote
47	2.1	393	2	B44767	L-mandelate dehydr
48	2.1	481	1	E54623	IMP dehydrogenase
49	2.1	481	1	H71890	IMP dehydrogenase
50	2.1	490	1	H70473	IMP dehydrogenase
51	2.1	521	1	T17196	IMP dehydrogenase
52	2.1	594	2	A75379	peptide ABC transp
53	2.1	1009	2	S26840	retrovirus-related
54	2.1	1009	2	S64734	retrovirus-related
55	1.8	91	2	G70238	hypothetical prote
56	1.8	96	2	E81047	hypothetical prote
57	1.8	104	2	B84037	thioredoxin trxa [
58	1.8	114	2	C81829	hypothetical prote
59	1.8	117	2	F87136	very hypothetical
60	1.8	135	2	C82821	NADH dehydrogenase
61	1.8	140	2	C71804	flagellar basal-bo
62	1.8	149	2	T03477	potential phosphat
63	1.8	153	2	A27179	collagen alpha 1(I
64	1.8	159	2	F82766	translation initia
65	1.8	166	2	A75383	hypothetical prote
66	1.8	179	2	C97117	signal peptidase I
67	1.8	187	2	G83243	peptidyl-prolyl ci
68	1.8	193	2	S39829	probable membrane
69	1.8	217	2	T46225	alpha NAC-like pro
70	1.8	217	2	D71866	hypothetical prote
71	1.8	222	2	C75539	conserved hypothet
72	1.8	224	2	S51579	cystathionine gamm
73	1.8	246	1	C72109	IMP dehydrogenase
74	1.8	246	2	D86512	inosine 5'-monopho
75	1.8	250	2	T04496	hypothetical prote
76	1.8	255	2	D71404	hypothetical prote
77	1.8	264	2	A12112	hypothetical prote
78	1.8	282	2	S50454	hypothetical prote
79	1.8	282	2	F64316	hypothetical prote
80	1.8	289	2	S16557	hypothetical prote
81	1.8	289	2	S16556	hypothetical prote
82	1.8	293	2	T50940	DiTD protein [imp
83	1.8	294	2	C82643	daunorubicin C-13
84	1.8	297	1	A30586	B-cell surface ant
85	1.8	299	1	A70118	glycine betaine, L
86	1.8	301	2	S28708	hypothetical prote
87	1.8	306	2	F64381	dihydroorotate oxi
88	1.8	307	2	G70665	hypothetical prote
89	1.8	308	2	AH2625	fructokinase [imp
90	1.8	311	2	S71228	O-succinylhomoseri
91	1.8	311	2	A86640	hypothetical prote
92	1.8	313	2	G97407	fructokinase [imp
93	1.8	319	2	S30173	probable mercuric
94	1.8	322	2	T31849	hypothetical prote
95	1.8	327	2	C91118	hypothetical prote
96	1.8	327	2	B85963	hypothetical prote
97	1.8	328	2	A82180	chemotaxis protein
98	1.8	332	2	I40726	rep protein - Cory
99	1.8	333	2	T06865	hypothetical prote
100	1.8	334	2	T12072	ABC-type permease

ALIGNMENTS

RESULT 1	
A35566	
IMP dehydrogenase (EC 1.1.1.205) I - human	
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate: dehydrogenas	
C:Species: Homo sapiens (man)	
C:Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 05-May-2000	
C:Accession: A35566	
R:Natsumeda, Y.; Ohno, S.; Kawasaki, H.; Konno, Y.; Weber, G.; Suzuki, K.	
J. Biol. Chem. 265, 5292-5295, 1990	
A:Title: Two distinct cDNAs for human IMP dehydrogenase.	
A:Reference number: A35566; MUID:90203022	
A:Accession: A35566	
A:Molecule type: mRNA	
A:Residues: 1-514 <NAT>	
A:Cross-references: GB:J05272; NID:g186393	
A:Note: the sequence in GenBank entry HUMIMPH, release 103, (PID:g307067) has 273-Phe, 2	
C:Comment: mRNA for IMP dehydrogenase I predominated in normal leukocytes, whereas that	
C:Genetics:	
A:Gene: GDB:IMPDH1; SWS2608	
A:Cross-references: GDB:128085; OMIM:146690	
A:Map position: 7q31.3-7q32	
C:Function:	
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule	
A:Pathway: purine nucleotide biosynthesis	
C:Superfamily: IMP dehydrogenase: CBS homology; IMP dehydrogenase amino-terminal homology	
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosyn	
F:30-96/Domain: IMP dehydrogenase amino-terminal homology <IDNH>	
F:117-168/Domain: CBS homology <CBS1>	
F:184-232/Domain: CBS homology <CBS2>	
F:233-476/Domain: IMP dehydrogenase catalytic homology <IDHC>	
F:331/Active site: Cys #status predicted	
Query Match 70.6%; Score 271; DB 1; Length 514;	
Best Local Similarity 100.0%; Pred. No. 4.3e-265;	
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 114	LLCGAAGTREDKRYDLDTQAGDVIVLDDSSQGSVYQIAMVHYIKQKYPHLQVIGGN 173
Db 244	LLCGAAGTREDKRYDLDTQAGDVIVLDDSSQGSVYQIAMVHYIKQKYPHLQVIGGN 303
QY 174	VVTAQAQKNLIDAGVGLRVMGCGSICITQEVMACGRPOGTAVYKVAEYARFVGPIIA 233
Db 304	VVTAQAQKNLIDAGVGLRVMGCGSICITQEVMACGRPOGTAVYKVAEYARFVGPIIA 363
QY 234	DGGIQTGVHVVKALALGASTVMGSLLAATTEAPGEYFFSDGVRLKKYRGMGSLDAMEKS 293
Db 364	DGGIQTGVHVVKALALGASTVMGSLLAATTEAPGEYFFSDGVRLKKYRGMGSLDAMEKS 423
QY 294	SSSQKRYFSGDKVKYTAQVSGSIQDKGSIQKFPVYLIAGIQHCCODIGARSLSVLRSM 353
Db 424	SSSQKRYFSGDKVKYTAQVSGSIQDKGSIQKFPVYLIAGIQHCCODIGARSLSVLRSM 483
QY 354	YSGELKFEKRTMSAQIEGGVHGLHSYEKRLY 384
Db 484	YSGELKFEKRTMSAQIEGGVHGLHSYEKRLY 514
RESULT 2	
A31997	
IMP dehydrogenase (EC 1.1.1.205) II - human	
N:Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH) type II	
C:Species: Homo sapiens (man)	
C:Date: 21-May-1990 #sequence_revision 22-May-1998 #text_change 16-Jul-1999	
C:Accession: I52303; I54184; A92676; B35566; A31997; A94550	
R:Giesne, D.A.; Huberman, E.	
Biochem. Biophys. Res. Commun. 205, 537-544, 1994	
A:Title: Cloning and sequence of the human type II IMP dehydrogenase gene.	
A:Reference number: I52303; MUID:95091778	
A:Accession: I52303	

A:Status: translated from GB/EMBL/DBDJ	
A:Molecule type: DNA	
A:Residues: 1-514 <GLE1>	
A:Cross-references: GB:I33842; NID:g602457; PIDN:AAA67054.1; PID:g602458	
R:Giesne, D.A.; Collart, F.R.; Varkony, T.; Drabkin, H.; Huberman, E.	
Genomics 16, 274-277, 1993	
A:Title: Chromosomal localization and structure of the human type II IMP dehydrogenas	
A:Reference number: I54184; MUID:93252398	
A:Accession: I54184	
A:Status: preliminary; translated from GB/EMBL/DBDJ	
A:Molecule type: DNA	
A:Residues: 461-514 <GLE2>	
A:Cross-references: GB:I08114; NID:g292239; PIDN:AAA36113.1; PID:g292240	
R:Collart, F.R.; Huberman, E.	
J. Biol. Chem. 263, 15769-15772, 1988	
A:Title: Cloning and sequence analysis of the human and Chinese hamster inosine-5'-mo	
A:Reference number: A92676; MUID:89008491	
A:Accession: A92676	
A:Molecule type: mRNA	
A:Residues: 1-189,'RS',192-514 <COL>	
A:Cross-references: GB:J04208; NID:g186391; PIDN:AAA36112.1; PID:g307066	
A:Note: submitted to the Protein Sequence Database, November 1989	
R:Natsumeda, Y.; Ohno, S.; Kawasaki, H.; Konno, Y.; Weber, G.; Suzuki, K.	
J. Biol. Chem. 265, 5292-5295, 1990	
A:Title: Two distinct cDNAs for human IMP dehydrogenase.	
A:Reference number: A35566; MUID:90203022	
A:Accession: B35566	
A:Status: nucleic acid sequence not shown; not compared with conceptual translation	
A:Molecule type: mRNA	
A:Residues: 1-514 <NAT>	
C:Comment: mRNA for IMP dehydrogenase I (see PIR:A35566) predominated in normal leuko	
C:Genetics:	
A:Gene: GDB:IMPDH2	
A:Cross-references: GDB:128086; OMIM:146691	
A:Map position: 3p24.2-3p21.2	
A:Introns: 33/2; 49/3; 83/3; 108/3; 177/3; 207/1; 274/1; 304/1; 336/1; 432/2; 480/2;	
C:Function:	
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecu	
A:Pathway: purine nucleotide biosynthesis	
C:Superfamily: IMP dehydrogenase: CBS homology; IMP dehydrogenase amino-terminal homo	
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis	
F:30-96/Domain: IMP dehydrogenase amino-terminal homology <IDNH>	
F:117-168/Domain: CBS homology <CBS1>	
F:184-232/Domain: CBS homology <CBS2>	
F:233-476/Domain: IMP dehydrogenase catalytic homology <IDHC>	
F:331/Active site: Cys #status predicted	
Query Match 8.1%; Score 31; DB 1; Length 514;	
Best Local Similarity 100.0%; Pred. No. 8.9e-23;	
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 245	KALALGASTVMGSLLAATTEAPGEYFFSDG 275
Db 375	KALALGASTVMGSLLAATTEAPGEYFFSDG 405
RESULT 3	
B31997	
IMP dehydrogenase (EC 1.1.1.205) - Chinese hamster	
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydroge	
C:Species: Crictetus griseus (Chinese hamster)	
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 05-May-2000	
A:Accession: B31997	
R:Collart, F.R.; Huberman, E.	
J. Biol. Chem. 263, 15769-15772, 1988	
A:Title: Cloning and sequence analysis of the human and Chinese hamster inosine-5'-mo	
A:Reference number: A92676; MUID:89008491	
A:Accession: B31997	
A:Molecule type: mRNA	
A:Residues: 1-514 <COL>	
A:Cross-references: GB:J04209; NID:g191119; PIDN:AAA36993.1; PID:g304517	
C:Function:	

A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of NADPH
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F:30-96/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:117-168/Domain: CBS homology <CBS1>
F:184-232/Domain: CBS homology <CBS2>
F:233-476/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:331/Active site: Cys #status predicted

Query Match 8.1%; Score 31; DB 1; Length 514;
Best Local Similarity 100.0%; Pred. No. 8.9e-23;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGASTVMGSLLAATTEAPGEYFFSDG 275
DB 375 KALALGASTVMGSLLAATTEAPGEYFFSDG 405

RESULT 4

IMP dehydrogenase (EC 1.1.1.205) - mouse
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydrogenase
C:Species: Mus musculus (house mouse)
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 05-May-2000
C:Accession: J0565; A34375; S42724
R:Tiedeman, A.A.; Smith, J.M.
Gene 97, 289-293, 1991

A:Title: Isolation and sequence of a cDNA encoding mouse IMP dehydrogenase.
A:Reference number: J0565; MUID:91153661
A:Accession: J0565

A:Molecule type: mRNA
A:Residues: 1-514 <TIE>
A:Cross-references: GB:M33934; NID:g198393; PIDN:AAA39311.1; PID:g309413
R:Hodges, S.D.; Fung, E.; McKay, D.J.; Renaux, B.S.; Snyder, F.F.
J. Biol. Chem. 264, 18137-18141, 1989

A:Title: Increased activity, amount, and altered kinetic properties of IMP dehydrogenase
A:Reference number: A34375; MUID:90036890
A:Accession: A34375

A:Molecule type: protein
A:Residues: 125-134;182-194;289-290;439-449;456-457, 'L',459-464, 'S',466;475-478 <HOD>
R:Lightfoot, T.; Snyder, F.F.
Biochim. Biophys. Acta 1217, 156-162, 1994

A:Title: Gene amplification and dual point mutations of mouse IMP dehydrogenase associated with the 129A mutation
A:Reference number: S42724; MUID:94153991
A:Accession: S42724

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA
A:Residues: 1-332, 'I',334-350, 'Y',352-482, 'M',484-514 <LIG>
A:Cross-references: EMBL:M98333; NID:g425157; PIDN:AAA20181.1; PID:g425158
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993

C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of NADPH
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F:30-96/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:117-168/Domain: CBS homology <CBS1>
F:184-232/Domain: CBS homology <CBS2>
F:233-476/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:331/Active site: Cys #status predicted

Query Match 8.1%; Score 31; DB 1; Length 514;
Best Local Similarity 100.0%; Pred. No. 8.9e-23;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGASTVMGSLLAATTEAPGEYFFSDG 275
DB 375 KALALGASTVMGSLLAATTEAPGEYFFSDG 405

RESULT 5

S41064
IMP dehydrogenase (EC 1.1.1.205) imph - fruit fly (Drosophila melanogaster)
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydrogenase
C:Species: Drosophila melanogaster
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 05-May-2000
C:Accession: S41064; S61482
R:Sifri, C.D.; Willson, K.; Smolik, S.; Forte, M.; Ullman, B.
Biochim. Biophys. Acta 1217, 103-106, 1994

A:Title: Cloning and sequence analysis of a Drosophila melanogaster cDNA encoding IMP dehydrogenase
A:Reference number: S41064; MUID:94114565
A:Accession: S41064

A:Molecule type: mRNA
A:Residues: 1-537 <SIF>
A:Cross-references: EMBL:L22608; NID:g348101; PIDN:AAA16839.1; PID:g348102
R:Nash, D.; Hu, S.; Leonard, N.J.; Tiong, S.Y.K.; Phillips, D.
Genome 37, 333-344, 1994

A:Title: The raspberry locus of Drosophila melanogaster includes an inosine monophosphatase
A:Reference number: S61482; MUID:94259281
A:Accession: S61482

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-537 <NAS>
C:Genetics:
A:Gene: imphd
A:Cross-references: FlyBase:FBgn0003204
A:Map position: 10
A:Introns: 55/2; 105/3; 323/1; 503/2

C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of NADPH
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F:52-118/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:139-189/Domain: CBS homology <CBS1>
F:203-231/Domain: CBS homology <CBS2>
F:252-499/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:350/Active site: Cys #status predicted

Query Match 6.0%; Score 23; DB 1; Length 537;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 EAPGEYFFSDGVRLKKYRGMSL 287
DB 414 EAPGEYFFSDGVRLKKYRGMSL 436

RESULT 6

S59508
IMP dehydrogenase (EC 1.1.1.205) ras - fruit fly (Drosophila sp.)
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydrogenase
C:Species: Drosophila sp.
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 05-May-2000
C:Accession: S59508
R:Slee, R.; Bownes, M.
Mol. Gen. Genet. 248, 755-766, 1995

A:Title: The raspberry locus encodes Drosophila inosine monophosphate dehydrogenase.
A:Reference number: S59508; MUID:96069715
A:Accession: S59508

A:Molecule type: mRNA
A:Residues: 1-537 <SLE>
A:Cross-references: GB:S80430; NID:gl245860; PIDN:AAB35628.1; PID:gl245861

C:Genetics:
A:Gene: FlyBase:ras
A:Cross-references: FlyBase:FBgn0003204
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of NADPH
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis

F:52-117/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:138-189/Domain: CBS homology <CBS1>
F:202-249/Domain: CBS homology <CBS2>
F:250-499/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:350/Active site: Cys #status Predicted

Query Match 6.0%; Score 23; DB 1; Length 537;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 EAPGEYFFSDGVRLLKKYRGMGSL 287
|||||
Db 414 EAPGEYFFSDGVRLLKKYRGMGSL 436

RESULT 7
S59402
IMP dehydrogenase (EC 1.1.1.205) YLR432w - yeast (Saccharomyces cerevisiae)
N:Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH); protein L9553.4
C:Species: Saccharomyces cerevisiae
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 23-Mar-2001
C:Accession: S59402

R:Du, Z.
submitted to the EMBL Data Library, February 1995
A:Description: The sequence of S. cerevisiae cosmid 9753.
A:Reference number: S53391

A:Accession: S59402

A:Molecule type: DNA

A:Residues: 1-523 <DUZ>

A:Cross-references: EMBL:U01094; NID:g665967; PIDN:AAB67516.1; PID:g665971; GSPDB:GN0001

A:Experimental source: strain S288C (AB972)

C:Genetics:

A:Gene: MIPS:YLR432w

A:Map position: 12R

C:Function:

A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of water
A:Pathway: purine nucleotide biosynthesis

C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology

C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis

F:37-103/Domain: IMP dehydrogenase amino-terminal homology <IDHN>

F:187-235/Domain: CBS homology <CBS>

F:236-484/Domain: IMP dehydrogenase catalytic homology <IDHC>

F:335/Active site: Cys #status Predicted

Query Match 5.5%; Score 21; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 GSICITQEVNACGRPGGTAVY 218
|||||
Db 332 GSICITQEVNACGRPGGTAVY 352

RESULT 8
S48997

IMP dehydrogenase (EC 1.1.1.205) PUR5 - yeast (Saccharomyces cerevisiae)
N:Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH); protein YHR216w

C:Species: Saccharomyces cerevisiae

C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 23-Mar-2001

C:Accession: S48997

R:Macri, C.

submitted to the EMBL Data Library, February 1994

A:Description: The sequence of S. cerevisiae cosmid 9177.

A:Reference number: S48997

A:Accession: S48997

A:Molecule type: DNA

A:Residues: 1-523 <MAC>

A:Cross-references: EMBL:U00029; NID:g551322; PIDN:AAB69728.1; PID:g458916; GSPDB:GN0000

A:Gene: PUR5; MIPS:YHR216w

A:Map position: 8R

C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of water
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F:37-103/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:187-235/Domain: CBS homology <CBS>
F:236-484/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:335/Active site: Cys #status Predicted

Query Match 5.5%; Score 21; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 GSICITQEVNACGRPGGTAVY 218
|||||
Db 332 GSICITQEVNACGRPGGTAVY 352

RESULT 9
S50890

IMP dehydrogenase (EC 1.1.1.205) YML056c - yeast (Saccharomyces cerevisiae)

N:Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH); protein YW958.06c

C:Species: Saccharomyces cerevisiae

C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000

C:Accession: S50890

R:Devlin, K.; Churcher, C.

submitted to the EMBL Data Library, November 1994

A:Reference number: S49800

A:Accession: S50890

A:Molecule type: DNA

A:Residues: 1-524 <DEV>

A:Cross-references: EMBL:Z46729; NID:g577134; PIDN:CAA86719.1; PID:g577140; GSPDB:GN0

C:Genetics:

A:Gene: MIPS:YML056c

A:Map position: 13L

A:Introns: 154/1

C:Function:

A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of water

A:Pathway: purine nucleotide biosynthesis

C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology

C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis

F:38-104/Domain: IMP dehydrogenase amino-terminal homology <IDHN>

F:188-236/Domain: CBS homology <CBS>

F:237-485/Domain: IMP dehydrogenase catalytic homology <IDHC>

F:336/Active site: Cys #status Predicted

Query Match 5.5%; Score 21; DB 1; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 GSICITQEVNACGRPGGTAVY 218
|||||
Db 333 GSICITQEVNACGRPGGTAVY 353

RESULT 10
JC7305

IMP dehydrogenase (EC 1.1.1.205) - Bacillus cereus

C:Species: Bacillus cereus

C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 24-Oct-2000

C:Accession: JC7305; PC7088

R:Kim, S. I.; Miyamoto, T.; Honjoh, K.; Iio, M.; Hatano, S.

Biosci. Biotechnol. Biochem. 64, 1210-1216, 2000

A:Title: Molecular cloning, overproduction and characterization of the Bacillus cereus

A:Reference number: JC7305

A:Accession: JC7305

A:Molecule type: DNA

A:Residues: 1-509 <KIM>

A:Cross-references: DDBJ:AB035643

A:Experimental source: strain ts-4

A:Accession: PC7088
 A:Molecule type: protein
 A:Residues: 1-7 <KI2>
 C:Genetics:
 A:Gene: impdh
 C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
 C:Keywords: DNA binding; GMP biosynthesis; NAD; oxidoreductase; sporulation
 F:308/Active site: Cys #status predicted

Query Match 3.6%; Score 14; DB 2; Length 509;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 MDTVTEADMAIAMA 83
 |||||
 Db 51 MDTVTEADMAIAMA 64

RESULT 11

T32709
 IMP dehydrogenase (EC 1.1.1.205) - Leishmania donovani
 N:Alternate names: IMPDH; inosine 5'-monophosphate dehydrogenase
 C:Species: Leishmania donovani
 C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 16-Jul-1999
 C:Accession: A38668
 R:Wilson, K.; Collart, F.R.; Huberman, E.; Stringer, J.R.; Ullman, B.
 J. Biol. Chem. 266: 1665-1671, 1991
 A:Title: Amplification and molecular cloning of the IMP dehydrogenase gene of Leishmania
 A:Reference number: A38668; MUID:91107664
 A:Accession: A38668
 A:Molecule type: DNA
 A:Residues: 1-514 <WIL>
 A:Cross-references: GB:M55667; NID:g159360
 C:Function:
 A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of
 A:Pathway: purine nucleotide biosynthesis
 C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
 C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
 F:28-94/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
 F:179-228/Domain: CBS homology <CBS>
 F:229-472/Domain: IMP dehydrogenase catalytic homology <IDHC>
 F:327/Active site: Cys #status predicted

Query Match 3.6%; Score 14; DB 1; Length 514;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 208 ACGRPGQTAVYKVA 221
 |||||
 Db 334 ACGRPGQTAVYKVA 347

RESULT 12

S53477
 IMP dehydrogenase (EC 1.1.1.205) FUN63 - yeast (Saccharomyces cerevisiae)
 N:Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH); protein YAR073w
 C:Species: Saccharomyces cerevisiae
 C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
 C:Accession: S53477
 R:Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; Kabac
 submitted to the EMBL Data Library, February 1994
 A:Description: Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of the
 A:Reference number: S53477
 A:Accession: S53477
 A:Molecule type: DNA
 A:Residues: 1-403 <BUS>
 A:Cross-references: EMBL:L28920; NID:g1616966; PIDN:AAC09509.1; PID:g456156; GSPDB:GN000
 C:Genetics:
 A:Gene: FUNG3; MIPS:YAR073w
 A:Map position: 1R
 C:Function:

A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecul
 A:Pathway: purine nucleotide biosynthesis
 C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
 C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
 F:37-103/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
 F:187-235/Domain: CBS homology <CBS>
 F:236-403/Domain: IMP dehydrogenase catalytic homology <IDHC>
 F:335/Active site: Cys #status predicted

Query Match 3.4%; Score 13; DB 1; Length 403;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 206 VMACGRPOGTAVY 218
 |||||
 Db 340 VMACGRPOGTAVY 352

RESULT 13

T32709
 IMP dehydrogenase (EC 1.1.1.205) T22D1.3 - Caenorhabditis elegans
 N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine 5'-monophosphate dehydroge
 C:Species: Caenorhabditis elegans
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
 C:Accession: T32709
 R:Geisel, C.; Bradshaw, H.; Hawkins, M.
 submitted to the EMBL Data Library, December 1997
 A:Description: The sequence of C. elegans cosmid T22D1.
 A:Reference number: T21211
 A:Accession: T32709
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-499 <GET>
 A:Cross-references: EMBL:AF039052; PIDN:AAB94282.1; GSPDB:GN000022; CESP:T22D1.3
 A:Experimental source: strain Bristol N2; clone T22D1
 C:Genetics:
 A:Gene: CESP:T22D1.3
 A:Map position: 4
 A:Introns: 35/2; 85/3; 159/1; 183/3; 342/1; 412/3; 493/2
 C:Function:
 A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecul
 A:Pathway: purine nucleotide biosynthesis
 C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
 C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide bio
 F:32-98/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
 F:120-170/Domain: CBS homology <CBS1>
 F:188-238/Domain: CBS homology <CBS2>
 F:239-461/Domain: IMP dehydrogenase catalytic homology <IDHC>
 F:337/Active site: Cys #status predicted

Query Match 3.4%; Score 13; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 0.00013;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 259 LLAATTEAPGEYF 271
 |||||
 Db 395 LLAATTEAPGEYF 407

RESULT 14

T40127
 IMP dehydrogenase (EC 1.1.1.205) SPBC2F12.14c - fission yeast (Schizosaccharomyces po
 N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine 5'-monophosphate dehydroge
 C:Species: Schizosaccharomyces pombe
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 21-Jul-2000
 C:Accession: T40127; T42083
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
 submitted to the EMBL Data Library, June 1997
 A:Reference number: T21907
 A:Accession: T40127
 A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-524 <MOO>
A:Cross-references: EMBL:Z97211; PIDN:CAB10161.1; GSPDB:GN00067; SPDB:SPBC2F12.14c
A:Experimental source: strain 972b-; cosmid c2f12
R:Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A:Reference number: Z17323; MUID:98162722
A:Accession: T42083
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 62-252, 'G', 254-262, 'P', 264-293 <YOS>
A:Cross-references: EMBL:D89106; NID:gl1749419; PIDN:RAA13769.1; PID:gl1749420
A:Experimental source: strain PR745
C:Genetics:
A:Gene: SPDB:SPBC2F12.14c
A:Map position: 2
A:Introns: 153/1
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosyn
F:37-103/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:124-174/Domain: CBS homology <CBS1>
F:187-237/Domain: CBS homology <CBS2>
F:238-486/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:337/Active site: Cys #status predicted

Query Match 3.4%; Score 13; DB 1; Length 524;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 CITQEVNACGRPQ 213
|||||
Db 337 CITQEVNACGRPQ 349

RESULT 15
F86298
IMP dehydrogenase (EC 1.1.1.205) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
C:Accession: F86298
R:Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: F86298
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-502 <STO>
A:Cross-references: GB:AE005172; NID:g4966356; PIDN:AAD34687.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
C:Keywords: GMP biosynthesis; NAD; oxidoreductase

Query Match 2.9%; Score 11; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 AGVDGLRVGMG 196
|||||
Db 306 AGVDGLRVGMG 316

RESULT 16
JC4999
IMP dehydrogenase (EC 1.1.1.205) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JC4999
R:Collart, F.R.; Osipiuk, J.; Trent, J.; Olsen, G.J.; Huberman, E.
Gene 174, 217-220, 1996
A:Title: Cloning and characterization of the gene encoding IMP dehydrogenase from Ara
A:Reference number: JC4999; MUID:97045815
A:Accession: JC4999
A:Molecule type: DNA
A:Residues: 1-503 <COL>
A:Cross-references: GB:L34684; NID:gl100062; PIDN:AAB41940.1; PID:gl1000063
C:Genetics:
A:Gene: impdh
A:Introns: 135/1; 334/3; 404/3; 490/3
C:Complex: homotetramer
C:Function:
A:Description: provides precursors for DNA and RNA biosynthesis; it catalyzes the con
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F:20-86/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:172-220/Domain: CBS homology <CBS2>
F:221-465/Domain: IMP dehydrogenase catalytic homology <IMP>
F:322/Active site: Cys #status predicted

Query Match 2.9%; Score 11; DB 1; Length 503;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 AGVDGLRVGMG 196
|||||
Db 307 AGVDGLRVGMG 317

RESULT 17
D83652
inositol-monophosphate dehydrogenase guaB [imported] - Bacillus halodurans (strain C-
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: D83652
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: D83652
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-485 <STO>
A:Cross-references: GB:AP001507; GB:BA000004; NID:gl0172612; PIDN:BA803739.1; GSPDB:G
A:Experimental source: strain C-125
C:Genetics:
A:Gene: guaB
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo

Query Match 2.6%; Score 10; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GVPITADGGI 237
|||||
Db 333 GVPITADGGI 342

RESULT 18
D97232
IMP dehydrogenase [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
 C:Accession: D97232
 R:Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum ATCC824
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: D97232
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-485 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AAK80647.1; PID:gl5025734; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC2701
 C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology

Query Match 2.6%; Score 10; DB 2; Length 485;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GVPITADGGI 237
 Db 331 GVPITADGGI 340
 |||||

RESULT 19
 H95270
 probable kinase/esterase [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid F
 C:Species: Sinorhizobium meliloti
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: H95270
 R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows, L.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
 A:Reference number: A95262; MUID:21396509; PMID:11481432
 A:Accession: H95270
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-742 <KUR>
 A:Cross-references: GB:AE006469; PIDN:AAK64730.1; PID:gl4523133; GSPDB:GN00165
 A:Experimental source: strain 1021, megaplasmid pSymA
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, F.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hymen, R.W.; Jones, T. Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: Sma0137
 A:Genome: plasmid

Query Match 2.6%; Score 10; DB 2; Length 742;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 ATAMALMGGI 88
 Db 27 ATAMALMGGI 36
 |||||

RESULT 20
 D72631
 probable IMP dehydrogenase (EC 1.1.1.205) APE1507 [similarity] - Aeropyrum pernix (strain N)
 N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; Inosine-5'-monophosphate dehydrogenase
 C:Species: Aeropyrum pernix
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 16-Jun-2000

C:Accession: D72631
 R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix
 A:Reference number: A72450; MUID:99310339
 A:Accession: D72631
 A:Molecule type: DNA
 A:Residues: 1-444 <KAW>
 A:Cross-references: DBJ:AP000061; NID:g5104821; PIDN:BAA80506.1; PID:g5105192
 A:Experimental source: strain K1
 C:Comment: This sequence is very similar to IMP dehydrogenase at the amino end and at the latter, the two CBS domains are missing or degenerate.
 C:Genetics:
 A:Gene: APE1507
 C:Superfamily: Lyme disease spirochete IMP dehydrogenase homolog; IMP dehydrogenase amino-terminal homology
 C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
 F:25-91/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
 F:174-417/Domain: IMP dehydrogenase catalytic homology <IDHC>
 F:271/Active site: Cys #status predicted

Query Match 2.3%; Score 9; DB 1; Length 444;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SSPMDTVTE 75
 Db 62 SSPMDTVTE 70
 |||||

RESULT 21
 C72264
 IMP dehydrogenase (EC 1.1.1.205) - Thermotoga maritima (strain MSB8)
 C:Species: Thermotoga maritima
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: C72264
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, J.; Nelson, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, C.M. Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 A:Reference number: A72200; MUID:99287316
 A:Accession: C72264
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-482 <ARN>
 A:Cross-references: GB:AE001789; GB:AE000512; NID:g4981904; PIDN:AAD36418.1; PID:g4981904
 A:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: TM1347
 C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
 C:Keywords: GMP biosynthesis; NAD; oxidoreductase
 F:5-71/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
 F:154-202/Domain: CBS homology <CBS>
 F:203-444/Domain: IMP dehydrogenase catalytic homology <IDC>
 F:301/Active site: Cys #status predicted

Query Match 2.3%; Score 9; DB 2; Length 482;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 VPIIADGGI 237
 Db 329 VPIIADGGI 337
 |||||

RESULT 22
 S54810
 probable oxygenase - Streptomyces fradiae
 C:Species: Streptomyces fradiae
 C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 24-Sep-1999

C;Accession: S54810
 R;Decker, H.; Haag, S.
 Submitted to the EMBL Data Library, May 1995
 A;Description: Cloning and characterization of a polyketide synthase from Streptomyces
 Y involved in its oxygenation.
 A;Reference number: S54810
 A;Accession: S54810
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-495 <DEC>
 A;Cross-references: EMBL: X87093; NID: g809102; PIDN: CAA60567.1; PID: g809103
 C;Superfamily: tetracycline 6-hydroxylase

Query Match 2.3%; Score 9; DB 2; Length 495;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 AGVDVIVLD 144
 |||||
 DB 24 AGVDVIVLD 32

RESULT 23
 G64501
 IMP dehydrogenase (EC 1.1.1.205) - Methanococcus jannaschii
 C;Species: Methanococcus jannaschii
 C;Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 21-Jul-2000
 C;Accession: G64501
 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
 A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A;Reference number: A64300; MUID: 96337999
 A;Accession: G64501
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-496 <BUL>
 A;Cross-references: GB: U67602; GB: L77117; NID: g1592214; PIDN: AAB99638.1; PID: g1592337;
 C;Genetics:
 A;Map position: FOR1591580-1593070
 A;Start codon: TTG
 C;Function:
 A;Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule
 A;Pathway: purine nucleotide biosynthesis
 C;Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
 C;Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosyn
 F;13-78/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
 F;99-147/Domain: CBS homology <CBS1>
 F;159-207/Domain: CBS homology <CBS2>
 F;208-458/Domain: IMP dehydrogenase catalytic homology <IDHC>
 F;306/Active site: Cys #status Predicted

Query Match 2.3%; Score 9; DB 1; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 VPIADGGI 237
 |||||
 DB 334 VPIADGGI 342

RESULT 24
 A55407
 IMP dehydrogenase (EC 1.1.1.205) - Trypanosoma brucei
 N;Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH)
 C;Species: Trypanosoma brucei
 C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 16-Jul-1999
 C;Accession: A55407
 R;Wilson, K.; Berens, R.L.; Sifri, C.D.; Ullman, B.

J. Biol. Chem. 269, 28979-28987, 1994
 A;Title: Amplification of the inosinate dehydrogenase gene in Trypanosoma brucei gamb
 A;Reference number: A55407; MUID: 95050714
 A;Accession: A55407
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-512 <WIL>
 A;Cross-references: GB: M97794; NID: g162135; PIDN: AAB46420.1; PID: g162136
 A;Note: authors translated the codon CGT for residue 76 as Leu
 C;Genetics:
 A;Gene: impdh
 C;Function:
 A;Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecul
 A;Pathway: purine nucleotide biosynthesis
 C;Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
 C;Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
 F;26-92/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
 F;177-226/Domain: CBS homology <CBS>
 F;227-470/Domain: IMP dehydrogenase catalytic homology <IDHC>
 F;325/Active site: Cys #status Predicted

Query Match 2.3%; Score 9; DB 1; Length 512;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SSPMDVTVE 75
 |||||
 DB 63 SSPMDVTVE 71

RESULT 25
 GNFG1
 retrovirus-related pol polyprotein homolog - fruit fly (Drosophila melanogaster) retr
 N;Contains: retropepsin (EC 3.4.23.16)
 C;Species: Drosophila melanogaster
 C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 16-Jul-1999
 C;Accession: B25666; A23769
 R;Marlor, R.L.; Parkhurst, S.M.; Corces, V.G.
 Mol. Cell. Biol. 6, 1129-1134, 1986
 A;Title: The Drosophila melanogaster gypsy transposable element encodes putative gene
 A;Reference number: A93071; MUID: 87064379
 A;Accession: B25666
 A;Molecule type: DNA
 A;Residues: 1-1035 <MAR>
 A;Note: the authors translated the codons CAG for residue 99 and CAA for residue 710
 R;Yuki, S.; Ishimaru, S.; Inouye, S.; Saigo, K.
 Nucleic Acids Res. 14, 3017-3030, 1986
 A;Title: Identification of genes for reverse transcriptase-like enzymes in two Drosop
 s.

A;Reference number: A23769; MUID: 86176782
 A;Accession: A23769
 A;Molecule type: DNA
 A;Residues: 21-30, 'AR', 33-59, 'R', 61-231, 'S', 233-489, 'V', 491-882, 'T', 884-922, 'S', 924-9
 A;Cross-references: GB: X03734; NID: g8036; PIDN: CAA27371.1; PID: g929567
 C;Genetics:
 A;Gene: FlyBase: gypsy/pol
 A;Cross-references: FlyBase: FBgn0014966
 C;Superfamily: pol polyprotein
 C;Keywords: aspartic proteinase; hydrolase; polyprotein; reverse transcriptase
 F;5-106/Product: retropepsin #status predicted <RTP>
 F;29/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 2.3%; Score 9; DB 1; Length 1035;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 LDLLTQAGV 138
 |||||
 DB 94 LDLLTQAGV 102


```

RESULT 26
H72054
Ribosomal protein S17 CP0109 [imported] - Chlamydomophila pneumoniae (strains CML029 and A
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: H72054; A81612
R:Kajman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606
A:Accession: H72054
A:Molecule type: DNA
A:Residues: 1-86 <ARN>
A:CROSS-references: GB:AE001647; GB:AE001363; NID:g4376920; PIDN:AAD18777.1; PID:g437693
A:Experimental source: strain CML029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255
A:Accession: A81612
A:Molecule type: DNA
A:Residues: 1-86 <REA>
A:CROSS-references: GB:AE002173; GB:AE002161; NID:g7189033; PIDN:AAF37992.1; PID:g718904
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: rs17; CP0109
C:Superfamily: Escherichia coli ribosomal protein S17

Query Match          2.1%; Score 8; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 SEGDKVKI 309
      |||||
DB 57 SEGDKVKI 64

RESULT 27
C86570
S17 ribosomal protein [imported] - Chlamydomophila pneumoniae (strain J138)
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: C86570
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; IS
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349
A:Accession: C86570
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86 <STO>
A:CROSS-references: GB:BA000008; NID:g8979010; PIDN:BAA98845.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: rs17

Query Match          2.1%; Score 8; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 SEGDKVKI 309
      |||||
DB 57 SEGDKVKI 64

RESULT 28
S78078
IMP dehydrogenase-related protein YAR075w - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Nov-1999

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C:Accession: S78078; S70312
R:Zhong, W.; Louis, E.J.; Bussey, H.
submitted to the EMBL Data Library, August 1996
A:Description: Saccharomyces cerevisiae chromosome I right arm.
A:Reference number: S78078
A:Accession: S78078
A:Molecule type: DNA
A:Residues: 1-157 <ZHO>
A:CROSS-references: EMBL:L28920; NID:g2911244; PID:g2911246; GSPDB:GN000001; MIPS:YARO
A:Note: this is a revision to the sequence from reference S53458
R:Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; Ka
submitted to the EMBL Data Library, February 1994
A:Description: Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of th
A:Reference number: S53458
A:Accession: S70312
A:Molecule type: DNA
A:Residues: 1-134 <BUS>
A:CROSS-references: EMBL:L28920; GSPDB:GN000001; MIPS:YAR075w
A:Note: This sequence has been revised in reference S78078
C:Comment: This sequence is highly similar to the carboxyl 30% of IMP dehydrogenase (
C:Genetics:
A:Gene: MIPS:YAR075w
A:Map position: 1R
C:Superfamily: hypothetical IMP dehydrogenase-related protein YAR075w; IMP dehydrogen
F:1-157/Domain: IMP dehydrogenase catalytic homology #status atypical <IDHC>

Query Match          2.1%; Score 8; DB 1; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 376 LHSYEKRL 383
      |||||
DB 148 LHSYEKRL 155

RESULT 29
AE0160
probable glutathione S-transferase-family protein YP01314 [imported] - Yersinia pesti
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AE0160
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB00001; MUID:21470413; PMID:11586360
A:Accession: AE0160
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-206 <KUR>
A:CROSS-references: GB:AL590842; PIDN:CAC90144.1; PID:g15979364; GSPDB:GN00175
C:Genetics:
A:Gene: YP01314
C:Superfamily: hypothetical protein b0838

Query Match          2.1%; Score 8; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 DKVKIAQG 312
      |||||
DB 124 DKVKIAQG 131

RESULT 30
C96948
deoxyphosphoglucanate aldolase (gene kdga) [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C:Accession: C96948

```

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daily, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum ATCC824
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: C96948
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-208 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK78374.1; PID:g15023245; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0394
C;Superfamily: 2-dehydro-3-deoxyphosphogluconate aldolase

Query Match 2.1%; Score 8; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 VVTAQAQK 181
|||||||
Db 71 VVTAQAQK 78

RESULT 31
S73185
hypothetical protein 254 - red alga (Porphyra purpurea) chloroplast
C;Species: chloroplast Porphyra purpurea
C;Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 24-Sep-1999
C;Accession: S73185
R;Reith, M.; Munnholland, J.
Plant Mol. Biol. Rep. 13, 333-335, 1995
A;Title: Complete nucleotide sequence of the Porphyra purpurea chloroplast genome.
A;Reference number: S73108
A;Accession: S73185
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-254 <REI>
A;Cross-references: EMBL:U38804; NID:g1276652; PIDN:AAC08150.1; PID:g1276730
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C;Genetics:
A;Genome: chloroplast
C;Superfamily: conserved hypothetical protein HI0188
C;Keywords: chloroplast

Query Match 2.1%; Score 8; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 APGEYFFS 273
|||||||
Db 78 APGEYFFS 85

RESULT 32
T09388
(S)-2-hydroxy-acid oxidase (EC 1.1.3.15) - alfalfa (fragment)
N;Alternate names: glycolate oxidase
C;Species: Medicago sativa (alfalfa)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Mar-2001
C;Accession: T09388
R;Stout, J.M.; McKersie, B.D.
submitted to the EMBL Data Library, August 1998
A;Description: Gene expression in alfalfa.
A;Reference number: Z14222
A;Accession: T09388
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-283 <STO>
A;Cross-references: EMBL:AF082874; NID:g3435305; PID:g3435306
A;Experimental source: shoot apical meristem

C;Function:
A;Description: catalyzes oxidation of glycolate to glyoxylate and hydrogen peroxide
A;Pathway: photorespiratory pathway
C;Superfamily: (S)-2-hydroxy-acid oxidase; (S)-2-hydroxy-acid oxidase homology
C;Keywords: flavoprotein; FMN; oxidoreductase; photorespiration
F;1-212/Domain: (S)-2-hydroxy-acid oxidase homology (fragment) <2HY>
F;166/Active site: His #status Predicted

Query Match 2.1%; Score 8; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGAS 252
|||||||
Db 208 KALALGAS 215

RESULT 33
T07032
(S)-2-hydroxy-acid oxidase (EC 1.1.3.15) - tomato (fragment)
N;Alternate names: glycolate oxidase
C;Species: Lycopersicon esculentum (tomato)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 18-Aug-2000
C;Accession: T07032
R;Speirs, J.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z15875
A;Accession: T07032
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-290 <SPE>
A;Cross-references: EMBL:X92888; NID:g1063399; PIDN:CAA63482.1; PID:g1063400
A;Experimental source: cultivar breeding line 'de Ruiter 83638'; Young leaf
C;Superfamily: (S)-2-hydroxy-acid oxidase; (S)-2-hydroxy-acid oxidase homology
C;Keywords: flavoprotein; FMN; oxidoreductase; photorespiration
F;1-220/Domain: (S)-2-hydroxy-acid oxidase homology (fragment) <2HY>
F;174/Active site: His #status Predicted

Query Match 2.1%; Score 8; DB 2; Length 290;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGAS 252
|||||||
Db 216 KALALGAS 223

RESULT 34
H96792
unknown protein F14G6.10 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: H96792
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maftl, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talloker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: H96792
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-302 <STO>
A;Cross-references: GB:AE005173; NID:g6642668; PIDN:AAF20248.1; GSPDB:GN00141
C;Genetics:
A;Gene: F14G6.10

A:Map position:11
C:Superfamily: Arabidopsis thaliana hypothetical protein T12H17.200

Query Match 2.1%; Score 8; DB 2; Length 302;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 QVIGGNV 175
|||||||
Db 197 QVIGGNV 204

RESULT 35
A71887
probable GMP reductase (EC 1.6.6.8) - Helicobacter pylori (strain J99)
N:Alternate names: guanosine monophosphate reductase
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 16-Jul-1999
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jlang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557
A:Accession: A71887
A:Molecule type: DNA
A:Residues: 1-325 <ARN>
A:CROSS-references: GB:AE001509; GB:AE001439; NID:94155350; PIDN:AAD06382.1; PID:9415537
C:Experimental source: strain J99
C:Genetics:
A:Gene: guac
C:Function:
A:Description: catalyzes the reductive deamination of GMP into IMP using NADPH
A:Pathway: purine catabolism
C:Superfamily: GMP reductase; IMP dehydrogenase amino-terminal homology; IMP dehydrogena
C:Keywords: NADP; oxidoreductase; purine catabolism
F:4-70/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:74-304/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:174/Active site: Cys #status predicted

Query Match 2.1%; Score 8; DB 1; Length 325;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 230 PIIADGGI 237
|||||||
Db 202 PIIADGGI 209

RESULT 36
C70015
probable GMP reductase (EC 1.6.6.8) yumd - Bacillus subtilis
N:Alternate names: guanosine monophosphate reductase
C:Species: Bacillus subtilis
C:Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 16-Jun-2000
C:Accession: C70015
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
A.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Pritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
ich, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsira, P.; Tognochi, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A:Reference number: A69580; MUID:98044033
A:Accession: C70015
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-326 <KUN>
A:CROSS-references: GB:299120; GB:AL009126; NID:g2635613; PIDN:CAB15203.1; PID:g26357
A:Experimental source: strain 168
C:Genetics:
A:Gene: yumd
C:Function:
A:Description: catalyzes the reductive deamination of GMP into IMP using NADPH
A:Pathway: purine catabolism
C:Superfamily: GMP reductase; IMP dehydrogenase amino-terminal homology; IMP dehydrog
C:Keywords: NADP; oxidoreductase; purine catabolism
F:5-71/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:75-305/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:175/Active site: Cys #status predicted

Query Match 2.1%; Score 8; DB 1; Length 326;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 230 PIIADGGI 237
|||||||
Db 203 PIIADGGI 210

RESULT 37
F64626
probable GMP reductase (EC 1.6.6.8) - Helicobacter pylori (strain 26695)
N:Alternate names: guanosine monophosphate reductase
C:Species: Helicobacter pylori
C:Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 16-Jul-1999
C:Accession: F64626
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; Mcke
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467
A:Accession: F64626
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-327 <TOM>
A:CROSS-references: GB:AE000596; GB:AE000511; NID:g2313982; PIDN:AAD07901.1; PID:g231
C:Function:
A:Description: catalyzes the reductive deamination of GMP into IMP using NADPH
A:Pathway: purine catabolism
C:Superfamily: GMP reductase; IMP dehydrogenase amino-terminal homology; IMP dehydrog
C:Keywords: NADP; oxidoreductase; purine catabolism
F:6-72/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:76-306/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:176/Active site: Cys #status predicted

Query Match 2.1%; Score 8; DB 1; Length 327;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 230 PIIADGGI 237
|||||||
Db 204 PIIADGGI 211

RESULT 38
D97326
GMP reductase [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C:Accession: D97326

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum ATCC824
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: D97326
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK81399.1; PID:g15026562; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
C:Superfamily: GMP reductase; IMP dehydrogenase amino-terminal homology; IMP dehydrogenase

Query Match 2.1%; Score 8; DB 2; Length 327;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 230 PIIADGGI 237
|||||||
Db 203 PIIADGGI 210

RESULT 39
A95145
conserved hypothetical protein SP1249 [imported] - Streptococcus pneumoniae (strain TIGR
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C:Accession: A95145
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: A95145
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-328 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK75354.1; PID:g14972731; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
C:Gene: SP1249
C:Superfamily: GMP reductase; IMP dehydrogenase amino-terminal homology; IMP dehydrogenase

Query Match 2.1%; Score 8; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 230 PIIADGGI 237
|||||||
Db 204 PIIADGGI 211

RESULT 40
G98012
GMP reductase [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C:Accession: G98012
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: G98012
A>Status: preliminary

A:Molecule type: DNA
A:Residues: 1-328 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAK99931.1; PID:g15458756; GSPDB:GN00174
C:Genetics:
A:Gene: guaC
C:Superfamily: GMP reductase; IMP dehydrogenase amino-terminal homology; IMP dehydrogenase

Query Match 2.1%; Score 8; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 230 PIIADGGI 237
|||||||
Db 204 PIIADGGI 211

Search completed: September 26, 2002, 08:34:44
Job time: 318 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2002, 08:32:22 ; Search time 13.39 Seconds
(without alignments)
1110.404 Million cell updates/sec

Title: US-09-853-918-30
Perfect score: 384
Sequence: 1 MADYLISGFGYVPEDGLTA.....MSAQIEGGVHGLHSYEKRLY 384

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	271	70.6	514	1	IMD1_HUMAN
2	87	22.7	514	1	IMD1_MOUSE
3	31	8.1	514	1	IMD2_HUMAN
4	31	8.1	514	1	IMD2_MESAU
5	31	8.1	514	1	IMD2_MOUSE
6	23	6.0	537	1	IMDH_DROME
7	21	5.5	521	1	IMH3_CANAL
8	21	5.5	523	1	IMH1_YEAST
9	21	5.5	523	1	IMH2_YEAST
10	21	5.5	524	1	IMH3_YEAST
11	14	3.6	514	1	IMDH_LEIDO
12	13	3.4	403	1	IMH4_YEAST
13	11	2.9	502	1	IMH2_ARATH
14	11	2.9	503	1	IMH1_ARATH
15	9	2.3	454	1	IMDH_PNECA
16	9	2.3	496	1	IMDH_METJA
17	9	2.3	512	1	IMDH_TRYBB
18	9	2.3	1035	1	POLY_DROME
19	8	2.1	86	1	RS17_CHLPN
20	8	2.1	254	1	YC43_PORPU
21	8	2.1	367	1	GOX1_ARATH
22	8	2.1	367	1	GOX2_ARATH
23	8	2.1	368	1	Y165_RICPR
24	8	2.1	393	1	MDLB_PSEPU
25	8	2.1	481	1	IMDH_HELPJ
26	8	2.1	481	1	IMDH_HELPY
27	8	2.1	490	1	IMDH_AQUAE
28	8	2.1	498	1	IMDH_RHTR
29	8	2.1	521	1	IMDH_CHLVI
30	7	1.8	163	1	Y22B_HAFIN
31	7	1.8	180	1	IF3_XYLFA
32	7	1.8	181	1	IF3_RHOSH
33	7	1.8	187	1	PP1A_PSEAE

34	7	1.8	193	1	YBF9_YEAST
35	7	1.8	227	1	MTR2_MOUSE
36	7	1.8	282	1	Y134_METJA
37	7	1.8	282	1	YEA5_YEAST
38	7	1.8	290	1	YCA3_GUTH
39	7	1.8	297	1	CD20_HUMAN
40	7	1.8	306	1	PYRD_METJA
41	7	1.8	319	1	MER4_STRLI
42	7	1.8	333	1	YC48_CYAPA
43	7	1.8	334	1	DMC1_YEAST
44	7	1.8	334	1	HMUU_YERPE
45	7	1.8	351	1	HAO2_HUMAN
46	7	1.8	352	1	HAO3_RAT
47	7	1.8	353	1	HAO3_HUMAN
48	7	1.8	369	1	GOX_SPIOL
49	7	1.8	370	1	HAO1_HUMAN
50	7	1.8	370	1	HAO1_MOUSE
51	7	1.8	384	1	FHUB_BACSU
52	7	1.8	404	1	IMDH_BORBU
53	7	1.8	405	1	AATC_RHIME
54	7	1.8	412	1	YG08_SYNY3
55	7	1.8	435	1	COBB_PSEAE
56	7	1.8	442	1	GLXD_RHIME
57	7	1.8	444	1	VGLX_HSVBS
58	7	1.8	457	1	CD4_MOUSE
59	7	1.8	466	1	BIAR_MOUSE
60	7	1.8	466	1	BIAR_RAT
61	7	1.8	467	1	BIAR_SHEEP
62	7	1.8	468	1	BIAR_PIG
63	7	1.8	473	1	BIAR_CANFA
64	7	1.8	474	1	BIAR_FELCA
65	7	1.8	485	1	IMDH_PYRAB
66	7	1.8	485	1	IMDH_PYRFU
67	7	1.8	486	1	IMDH_PYRHO
68	7	1.8	487	1	IMDH_PASMU
69	7	1.8	488	1	IMDH_ACICA
70	7	1.8	488	1	IMDH_ECOLI
71	7	1.8	488	1	IMDH_HAEIN
72	7	1.8	491	1	GABD_RHISN
73	7	1.8	492	1	IMDH_STRPY
74	7	1.8	513	1	IMDH_BACSU
75	7	1.8	528	1	YC79_MYCTU
76	7	1.8	529	1	IMDH_MYCLE
77	7	1.8	529	1	IMDH_MYCTU
78	7	1.8	549	1	BETA_RHIME
79	7	1.8	559	1	RS1_BUCAP
80	7	1.8	561	1	EST1_MESAU
81	7	1.8	563	1	METB_ARATH
82	7	1.8	571	1	UVRC_MYCBV
83	7	1.8	614	1	BTUB_SALTY
84	7	1.8	614	1	SPKE_SYNY3
85	7	1.8	700	1	PALY_WHEAT
86	7	1.8	700	1	YNCB_ECOLI
87	7	1.8	770	1	ACE2_YEAST
88	7	1.8	811	1	MUTS_THAEQ
89	7	1.8	824	1	NSFH_CAEEL
90	7	1.8	902	1	SYG1_YEAST
91	7	1.8	917	1	GLRK_LYMST
92	7	1.8	946	1	K6P2_CANAL
93	7	1.8	1025	1	MK21_YEAST
94	7	1.8	1032	1	Y895_HAEIN
95	7	1.8	1128	1	NGP1_HUMAN
96	7	1.8	1128	1	NGP1_RAT
97	7	1.8	1453	1	CAL1_CHICK
98	7	1.8	1569	1	YFJA_ECOLI
99	7	1.8	2284	1	POLI_GFLV
100	7	1.8	2747	1	FAP_DROME

ALIGNMENTS

RESULT 1

KW Multigene family; Repeat; CBS domain.
 FT DOMAIN 112 167 CBS 1.
 FT BINDING 177 232 CBS 2.
 FT BINDING 331 331 IMP (POTENTIAL).
 SQ SEQUENCE 514 AA; 55294 MW; B38AA2EB0ECC4CE CRC64;

Query Match 22.7%; Score 87; DB 1; Length 514;
 Best Local Similarity 100.0%; Pred. No. 7.2e-78;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 DSSQNSVYQIAMVHIKQYKYPHLQVIGNVVTAQAQKNLIDAGVDGLRVGMCSSICIT 203
 |||||
 DB 274 DSSQNSVYQIAMVHIKQYKYPHLQVIGNVVTAQAQKNLIDAGVDGLRVGMCSSICIT 333
 |||||

QY 204 QEVMAQGRPGQTAVYKVAEYARFGVP 230
 |||||
 DB 334 QEVMAQGRPGQTAVYKVAEYARFGVP 360
 |||||

RESULT 3
 IMD2_HUMAN
 ID IMD2_HUMAN STANDARD; PRT; 514 AA.
 AC P12268;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inosine-5'-monophosphate dehydrogenase 2 (EC 1.1.1.205) (IMP
 dehydrogenase 2) (IMPDH-II) (IMPD 2).
 GN IMPDH2 OR IMPD2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=89008491; PubMed=2902093;
 RA Collart F.R., Huberman E.;
 RT "Cloning and sequence analysis of the human and Chinese hamster
 RT inosine-5'-monophosphate dehydrogenase cDNAs.";
 RL J. Biol. Chem. 263:15769-15772(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=90203022; PubMed=1969416;
 RA Natsumeda Y., Ohno S., Kawasaki H., Konno Y., Weber G., Suzuki K.;
 RT "Two distinct cDNAs for human IMP dehydrogenase.";
 RL J. Biol. Chem. 265:5292-5295(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=95091778; PubMed=7999076;
 RA Glesne D.A., Huberman E.;
 RT "Cloning and sequence of the human type II IMP dehydrogenase gene.";
 RL Biochem. Biophys. Res. Commun. 205:537-544(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95204479; PubMed=7896827;
 RA Zimmermann A.G., Spychala J., Mitchell B.S.;
 RT "Characterization of the human inosine-5'-monophosphate dehydrogenase
 RT type II gene.";
 RL J. Biol. Chem. 270:6808-6814(1995).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE=95283610; PubMed=7763314;
 RA Hager P.W., Collart F.R., Huberman E., Mitchell B.S.;
 RT "Recombinant human inosine monophosphate dehydrogenase type I and
 RT type II proteins. Purification and characterization of inhibitor
 RT binding.";
 RL Biochem. Pharmacol. 49:1323-1329(1995).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=99199217; PubMed=10097070;

RA Colby T.D., Vanderveen K., Strickler M.D., Markham G.D.,
 RA Goldstein B.M.;
 RT "Crystal structure of human type II inosine monophosphate
 RT dehydrogenase: Implications for ligand binding and drug design.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:3531-3536(1999).
 CC -!- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
 CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
 CC OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF
 CC MALIGNANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.
 CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
 CC xanthosine 5'-phosphate + NADH.
 CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
 CC -!- SUBUNIT: HOMOTETRAMER.
 CC -!- TISSUE SPECIFICITY: IMP TYPE I IS THE MAIN SPECIES IN NORMAL
 CC LEUKOCYTES AND TYPE II PREDOMINATES OVER TYPE I IN THE TUMOR.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 CC GMP REDUCTASE.
 CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
 CC -----
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 CC -----
 CC EMBL; J04208; AAA36112.1; -;
 CC EMBL; L33842; AAA67054.1; -;
 CC EMBL; L39210; AAB70699.1; -;
 CC PIR; A31997; A31997.
 CC PIR; B35566; B35566.
 CC PDB; 1B30; 12-APR-99.
 CC MIM; 146691; -;
 CC InterPro; IPR000644; CBS.
 CC InterPro; IPR003009; FMN_enzyme.
 CC InterPro; IPR001093; IMP_DH_GMP_RED.
 CC Pfam; PF00571; CBS; 2.
 CC Pfam; PF00478; IMPDH_C; 1.
 CC Pfam; PF01574; IMPDH_N; 1.
 CC SMART; SM00116; CBS; 2.
 CC PROSITE; PS00487; IMP_DH_GMP_RED; 1.
 CC Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
 KW Multigene family; Repeat; CBS domain; 3D-structure.
 FT DOMAIN 112 167 CBS 1.
 FT BINDING 177 232 CBS 2.
 FT BINDING 331 331 IMP (POTENTIAL).
 FT CONFLICT 190 191 AG -> RS (IN REF. 1).
 SQ SEQUENCE 514 AA; 55805 MW; 876BEA0EC1DDBEE9 CRC64;

Query Match 8.1%; Score 31; DB 1; Length 514;
 Best Local Similarity 100.0%; Pred. No. 1.4e-22;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGASTVMGMSLLAATTEAPGEYFFSDG 275
 |||||
 DB 375 KALALGASTVMGMSLLAATTEAPGEYFFSDG 405
 |||||

RESULT 4
 IMD2_MESAU
 ID IMD2_MESAU STANDARD; PRT; 514 AA.
 AC P12269;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Inosine-5'-monophosphate dehydrogenase 2 (EC 1.1.1.205) (IMP
 dehydrogenase 2) (IMPDH-II) (IMPD 2).
 GN IMPDH2 OR IMPDH.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 336-370.
 RX MEDLINE=89008491; PubMed=2902093;
 RA Collart F.R., Huberman E.;
 RT "Cloning and sequence analysis of the human and Chinese hamster
 RT Inosine-5'-monophosphate dehydrogenase cDNAs.";
 RL J. Biol. Chem. 263:15769-15772(1988).
 CC -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
 CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
 CC OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF
 CC MALIGNANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.
 CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
 CC xanthosine 5'-phosphate + NADH.
 CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 CC GMP REDUCTASE.
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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 CC -----
 DR EMBL; J04209; AAA36993.1; -;
 DR PIR; B31997; B31997.
 DR HSSP; P12268; 1B30.
 DR InterPro; IPR000644; CBS.
 DR InterPro; IPR003009; FMN enzyme.
 DR InterPro; IPR001093; IMP_DH_GMP_RED.
 DR Pfam; PF00571; CBS; 2.
 DR Pfam; PF00478; IMPDH_C; 1.
 DR Pfam; PF01574; IMPDH_N; 1.
 DR SMART; SM00116; CBS; 2.
 DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
 KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
 KW Multigene family; Repeat; CBS domain.
 FT DOMAIN 112 167
 FT BINDING 177 232 CBS 2.
 FT VARIANT 331 333 IMP (POTENTIAL).
 FT BINDING 331 333 IMP (POTENTIAL).
 FT VARIANT 331 333
 FT VARIANT 351 351
 FT CONFLICT 483 483 T -> M (IN REF. 2).
 SQ SEQUENCE 514 AA; 55890 MW; 5FA0138FA41E8A02 CRC64;
 Query Match 8.1%; Score 31; DB 1; Length 514;
 Best Local Similarity 100.0%; Pred. No. 1.4e-22;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 245 KALALGASTVMMGSLAATTEAPGEYFFSDG 275
 Db 375 KALALGASTVMMGSLAATTEAPGEYFFSDG 405
 RESULT 5
 IMD2_MOUSE
 ID IMD2_MOUSE STANDARD; PRT; 514 AA.
 AC P24547; Q61734;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Inosine-5'-monophosphate dehydrogenase 2 (EC 1.1.1.205) (IMP
 DE dehydrogenase 2) (IMPDH-II) (IMPD 2).
 GN IMPDH2 OR IMPDH.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=91153661; PubMed=1671845;
 RA Tiedeman A.A., Smith J.M.;
 RT "Isolation and sequence of a cDNA encoding mouse IMP dehydrogenase.";
 RL Gene 97:289-293(1991).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANTS MYCOPHENOLIC ACID RESISTANT.
 RC TISSUE=Brain;
 RX MEDLINE=94153991; PubMed=7906545;
 RA Lightfoot T., Snyder F.F.;
 RT "Gene amplification and dual point mutations of mouse IMP
 RT dehydrogenase associated with cellular resistance to mycophenolic
 RT acid.";
 RL Biochim. Biophys. Acta 1217:156-162(1994).
 CC -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
 CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
 CC OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF
 CC MALIGNANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.
 CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
 CC xanthosine 5'-phosphate + NADH.
 CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 CC GMP REDUCTASE.
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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 CC -----
 DR EMBL; M33934; AAA39311.1; -;
 DR PIR; M98333; AAA20181.1; -;
 DR PIR; JT0565; JT0565.
 DR HSSP; P12268; 1B30.
 DR MGD; MGI:109367; Impdh2.
 DR InterPro; IPR000644; CBS.
 DR InterPro; IPR003009; FMN enzyme.
 DR InterPro; IPR001093; IMP_DH_GMP_RED.
 DR Pfam; PF00571; CBS; 2.
 DR Pfam; PF00478; IMPDH_C; 1.
 DR Pfam; PF01574; IMPDH_N; 1.
 DR SMART; SM00116; CBS; 2.
 DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
 KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
 KW Multigene family; Repeat; CBS domain.
 FT DOMAIN 112 167
 FT BINDING 177 232 CBS 2.
 FT BINDING 331 331 IMP (POTENTIAL).
 FT VARIANT 333 333 T -> I (IN MYCOPHENOLIC ACID RESISTANT
 FT CELLS).
 FT VARIANT 351 351 S -> Y (IN MYCOPHENOLIC ACID RESISTANT
 FT CELLS).
 FT CONFLICT 483 483 T -> M (IN REF. 2).
 SQ SEQUENCE 514 AA; 55785 MW; D5B66A5C5EBC421 CRC64;
 Query Match 8.1%; Score 31; DB 1; Length 514;
 Best Local Similarity 100.0%; Pred. No. 1.4e-22;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 245 KALALGASTVMMGSLAATTEAPGEYFFSDG 275
 Db 375 KALALGASTVMMGSLAATTEAPGEYFFSDG 405
 RESULT 6
 IMDH_DROME
 ID IMDH_DROME STANDARD; PRT; 537 AA.
 AC Q07152; Q26455; Q9W2R8;

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
 DE dehydrogenase) (IMPDH) (IMPD) (Raspberry protein).
 GN RAS OR CGI799.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RP [1]
 RP SEQUENCE FROM N.A.
 RA Nash D., Hu S.;
 RT "Drosophila inosine monophosphate dehydrogenase is encoded at the
 RT raspberry locus";
 RL (In) Abstracts of the 35th meeting of the Canadian Federation of
 RL Biological Societies, pp.72-72, Victoria (1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94259281; PubMed=7911114;
 RA Nash D., Hu S., Leonard N.J., Tjong S.Y., Phillips D.;
 RT "The raspberry locus of Drosophila melanogaster includes an inosine
 RT monophosphate dehydrogenase like coding sequence.";
 RL Genome 37:333-344(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CANTON-S;
 RX MEDLINE=94114565; PubMed=7904480;
 RA Sifri C.D., Wilson K., Smolik S., Forte M., Ullman B.;
 RT "Cloning and sequence analysis of a Drosophila melanogaster cDNA
 RT encoding IMP dehydrogenase";
 RL Biochim. Biophys. Acta 1217:103-106(1994).
 RN [4]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=96069715; PubMed=7476879;
 RA Sile R., Bowles M.;
 RT "The raspberry locus encodes Drosophila inosine monophosphate
 RT dehydrogenase";
 RL Mol. Gen. Genet. 248:755-766(1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pohlard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RL "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
 CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
 CC OF CELL GROWTH.
 CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
 CC xanthosine 5'-phosphate + NADH.
 CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
 CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 CC GMP REDUCTASE.
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
 CC -----
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 CC -----
 DR EMBL; L14847; AAA21831.1; -;
 DR EMBL; L22608; AAA16839.1; -;
 DR EMBL; S80430; AAB35628.1; -;
 DR EMBL; AE003451; AAF46622.1; -;
 DR HSSP; P12268; 1B30.
 DR FlyBase; FBgn0003204; ras.
 DR InterPro; IPR000644; CBS.
 DR InterPro; IPR003009; FMN_enzyme.
 DR InterPro; IPR01093; IMP_DH_GMP_RED.
 DR Pfam; PF00571; CBS; 2.
 DR Pfam; PF00478; IMPDH_C; 1.
 DR Pfam; PF01574; IMPDH_N; 1.
 DR SMART; SM00116; CBS; 2.
 DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
 KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
 KW CBS domain.
 FT DOMAIN 134 189 CBS 1.
 FT DOMAIN 198 251 CBS 2.
 FT BINDING 350 350 IMP (BY SIMILARITY).
 FT CONFLICT 38 38 D -> V (IN REF. 4).
 FT CONFLICT 53 53 T -> P (IN REF. 4).
 FT CONFLICT 99 102 EMAL -> RCH (IN REF. 4).
 FT CONFLICT 184 184 D -> A (IN REF. 4).
 FT CONFLICT 194 194 V -> S (IN REF. 4).
 FT CONFLICT 216 217 AN -> EH (IN REF. 4).
 FT CONFLICT 226 229 GKLP -> ATA (IN REF. 4).
 FT CONFLICT 244 244 T -> A (IN REF. 4).
 FT CONFLICT 261 262 KO -> TR (IN REF. 4).
 FT CONFLICT 265 266 VG -> CP (IN REF. 4).
 FT CONFLICT 277 278 AR -> GCRA (IN REF. 4).
 FT CONFLICT 284 284 A -> R (IN REF. 4).
 FT CONFLICT 301 301 Y -> I (IN REF. 4).
 FT CONFLICT 387 388 QS -> HA (IN REF. 4).
 SQ SEQUENCE 537 AA; 57829 MW; A5EAB41AEAA64EBD CRC64;
 Query Match 6.0%; Score 23; DB 1; Length 537;
 Best Local Similarity 100.0%; Pred.No. 1.2e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 265 EAPGEYFFSDGVRLLKRYGMGSL 287
 Db 414 EAPGEYFFSDGVRLLKRYGMGSL 436
 RESULT 7

IMH3_CANAL
ID IMH3_CANAL STANDARD; PRT; 521 AA.
AC O00086;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
dehydrogenase) (IMPDH) (IMPD).
GN IMH3.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=3476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SS;
RX MEDLINE=97234646; PubMed=9079920;
RA Koehler G.A., White T.C., Agabian N.;
RT "overexpression of a cloned IMP dehydrogenase gene of Candida
albicans confers resistance to the specific inhibitor mycophenolic
acid.";
RL J. Bacteriol. 179:2331-2338(1997).
CC -1- FUNCTION: ESSENTIAL ENZYME IN THE DE NOVO BIOSYNTHESIS OF GMP,
CATALYSING THE NAD-DEPENDENT OXIDATION OF IMP TO XMP.
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT EQUAL LEVELS IN THE YEAST OR
HYPHAL FORM.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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CC
CC EMBL; U85049; AAB51509.1; -
DR HSSP; P12268; LB30.
DR COMPLEYEAST-2DPAGE; O00086; -
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain.
FT DOMAIN 117 172 CBS 1.
FT DOMAIN 180 232 CBS 2.
FT BINDING 333 333 IMP (POTENTIAL).
SQ SEQUENCE 521 AA; 56239 MW; 5F1E52611B1E1418 CRC64;

Query Match 5.5%; Score 21; DB 1; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 GSICITQEVNACGRPGGTAVY 218
|||||
Db 330 GSICITQEVNACGRPGGTAVY 350

RESULT 8
IMH1_YEAST
ID IMH1_YEAST STANDARD; PRT; 523 AA.
AC P38697;

DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
dehydrogenase) (IMPDH) (IMPD).
GN PUR5 OR YHR216W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetales; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Willcox L., Wohlman P., Waterston R., Wilson R.,
Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
VIII.";
RL Science 265:2077-2082(1994).
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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CC
CC EMBL; U00029; AAB69728.1; -
DR PIR; S48997; S48997.
DR HSSP; P12268; LB30.
DR SGD; S0001259; PUR5.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
KW Multigene family; Repeat; CBS domain.
FT DOMAIN 119 174 CBS 1.
FT DOMAIN 182 234 CBS 2.
FT BINDING 335 335 IMP (POTENTIAL).
SQ SEQUENCE 523 AA; 56530 MW; 7CA3EC11238906B9 CRC64;

Query Match 5.5%; Score 21; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 GSICITQEVNACGRPGGTAVY 218
|||||
Db 332 GSICITQEVNACGRPGGTAVY 352

RESULT 9
IMH2_YEAST
ID IMH2_YEAST STANDARD; PRT; 523 AA.
AC P50095;
DT 01-OCT-1996 (Rel. 34, Created)

```
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN YLR432W OR L3753.4.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favetto A., Fulton L., Gattung S., Greco T., Kirsten J.,
RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
RA Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
RA Mardis E., Meneses S., Miller N., Nhan M., Pauley A., Peluso D.,
RA Rifken L., Riles L., Taich A., Trevaskis E., Vignati D.,
RA Wilcox L., Wohlman P., Vaudin M., Wilson R., Waterston R.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U21094; AB67516.1; -.
DR HSSP: P12268; 1B30.
DR SGD: S0004424; YLR432W.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR SMART: SM00116; IMPDH_N; 1.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
DR Hypothetical protein; Oxidoreductase; NAD; GMP biosynthesis;
KW Purine biosynthesis; Multigene family; Repeat; CBS domain.
FT DOMAIN 119 174 CBS 1.
FT DOMAIN 182 234 CBS 2.
FT BINDING 335 335 IMP (POTENTIAL).
SQ SEQUENCE 523 AA; 56584 MW; A0C84C225277AAE6 CRC64;

Query Match 5.5%; Score 21; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 198 GSICITQEVMACGRPGQTAVY 218
Db 332 GSICITQEVMACGRPGQTAVY 352

RESULT 10
IMH3_YEAST
ID IMH3_YEAST STANDARD; PRT; 524 AA.
AC P50094;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN YML056C OR YM9958.06C.
```

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OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Devlin K., Churcher C., Barrell B.G., Rajandream M.A.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z46729; CAAB6719.1; -.
DR HSSP: P12268; 1B30.
DR SGD: S0004520; YML056C.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
DR Hypothetical protein; Oxidoreductase; NAD; GMP biosynthesis;
KW Purine biosynthesis; Multigene family; Repeat; CBS domain.
FT DOMAIN 120 175 CBS 1.
FT DOMAIN 183 235 CBS 2.
FT BINDING 336 336 IMP (POTENTIAL).
SQ SEQUENCE 524 AA; 56394 MW; A73D1E4EFE8AEAD9 CRC64;

Query Match 5.5%; Score 21; DB 1; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 198 GSICITQEVMACGRPGQTAVY 218
Db 333 GSICITQEVMACGRPGQTAVY 353

RESULT 11
IMDH_LEIDO
ID IMDH_LEIDO STANDARD; PRT; 514 AA.
AC P21620;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
OC Leishmania donovani.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5661;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=91107664; PubMed=1671039;
RA Wilson K.E., Collart F.R., Huberman E., Stringer J.R., Ullman B.;
RT "Amplification and molecular cloning of the IMP dehydrogenase gene of
RT Leishmania donovani."
RL J. Biol. Chem. 266:1665-1671(1991).
CC -!- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
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CC      -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; L28920; AAC09509.1; -.
CC      DR      HSSP; P12268; 1B30.
CC      DR      SGD; S0000095; YAR073W.
CC      DR      InterPro; IPR000644; CBS.
CC      DR      InterPro; IPR001093; IMP_DH_GMP_RED.
CC      DR      Pfam; PF00571; CBS; 2.
CC      DR      Pfam; PF00478; IMPDH_C; 1.
CC      DR      Pfam; PF01574; IMPDH_N; 1.
CC      DR      SMART; SM00116; CBS; 2.
CC      DR      PROSITE; PS00487; IMP_DH_GMP_RED; 1.
CC      KW      Hypothetical protein; Oxidoreductase; NAD; GMP biosynthesis;
CC      KW      Purine biosynthesis; Multigene family; Repeat; CBS domain.
CC      FT      DOMAIN 119 174 CBS 1.
CC      FT      DOMAIN 182 235 CBS 2.
CC      FT      BINDING 335 335 IMP (POTENTIAL).
CC      SQ      SEQUENCE 403 AA; 44386 MW; F6BC13E46D5D1ECD CRC64;
CC
CC      Query Match 3.4%; Score 13; DB 1; Length 403;
CC      Best Local Similarity 100.0%; Pred. No. 6.7e-05;
CC      Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC      QY 206 VMACGRPGGTAVY 218

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RESULT 13
IMH2_ARATH STANDARD; PRP; 502 AA.
ID IMH2_ARATH STANDARD; PRP; 502 AA.
AC Q9SA34;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN ATG16350 OR F309.15.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxId=3702;
[1]
SEQUENCE FROM N.A.
RN
RP
RC STRAIN=CV, COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Elgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizier L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Millscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Tortum M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "sequence and analysis of chromosome 1 of the plant Arabidopsis

```

RT thaliana.";
RL Nature 408:816-820(2000).
CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC
CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC
CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC
CC -!- SIMILARITY: CONTAINS 1 CBS DOMAIN.
CC
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CC
CC -----
CC EMBL; AC006341; AAD34687.1; -.
CC HSSP; P12268; 1B30.
CC InterPro; IPR000644; CBS.
CC InterPro; IPR003009; FMN_enzyme.
CC InterPro; IPR001093; IMP_DH_GMP_RED.
CC Pfam; PF00571; CBS; 1.
CC Pfam; PF00478; IMPDH_C; 1.
CC Pfam; PF01574; IMPDH_N; 1.
CC PROSITE; PS00487; IMP_DH_GMP_RED; 1.
CC Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
CC CBS domain. 167 219
CC DOMAIN 321 322 IMP (POTENTIAL).
CC FT BINDING 321 322
CC SEQUENCE 502 AA; 54051 MW; FB87D84160818310 CRC64;

Query Match 2.9%; Score 11; DB 1; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 AGVDGLRVGMG 196
DB 306 AGVDGLRVGMG 316
|||||
306 AGVDGLRVGMG 316

RESULT 14
IMH1_ARATH
ID IMH1_ARATH STANDARD; PRT; 503 AA.
AC P47996;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN IMPDH OR AT1G79470 OR T8K14.11.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=97045815; PubMed=8990737;
RA Collart F.R., Osipiuk J., Trent J., Olsen G.J., Huberman E.;
RT "Cloning and characterization of the gene encoding IMP dehydrogenase
RT from Arabidopsis thaliana.";
RL Gene 174:217-220(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

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RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Malti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC
CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC
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CC
CC -----
CC EMBL; L34684; AAB41940.1; -.
CC EMBL; AC007202; AAD30229.1; -.
CC HSSP; P12268; 1B30.
CC InterPro; IPR000644; CBS.
CC InterPro; IPR003009; FMN_enzyme.
CC InterPro; IPR001093; IMP_DH_GMP_RED.
CC Pfam; PF00571; CBS; 1.
CC Pfam; PF00478; IMPDH_C; 1.
CC Pfam; PF01574; IMPDH_N; 1.
CC PROSITE; PS00487; IMP_DH_GMP_RED; 1.
CC Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain. 322 322 IMP (POTENTIAL).
FT BINDING 322 322
SQ SEQUENCE 503 AA; 54194 MW; ADDDAF9C3A697A9A CRC64;

Query Match 2.9%; Score 11; DB 1; Length 503;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 AGVDGLRVGMG 196
DB 307 AGVDGLRVGMG 317
|||||
307 AGVDGLRVGMG 317

RESULT 15
IMDH_PNECA
ID IMDH_PNECA STANDARD; PRT; 454 AA.
AC Q12658;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN GUAL.
OS Pneumocystis carinii.
OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OX NCBI_TaxID=4754;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97135213; PubMed=8980752;
RA O'Gara M.J., Lee C.H., Weinberg G.A., Nott J.M., Queener S.F.;

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CC  -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC  GMP REDUCTASE.
CC  -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; M97794; AAB46420.1; -.
DR  HSSP; P12268; LB30.
DR  InterPro; IPR000644; CBS.
DR  InterPro; IPR003009; FMN_enzyme.
DR  InterPro; IPR001093; IMP_DH_GMP_RED.
DR  Pfam; PF00571; CBS; 2.
DR  Pfam; PF00478; IMPDH_C; 1.
DR  Pfam; PF01574; IMPDH_N; 1.
DR  SMART; SM00116; CBS; 2.
DR  PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW  Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW  CBS domain.
FT  DOMAIN 108 163 CBS 1.
FT  DOMAIN 170 226 CBS 2.
FT  BINDING 325 325 IMP (POTENTIAL).
SQ  SEQUENCE 512 AA; 55708 MW; 1A86C46AE6445045 CRC64;

Query Match 2.3%; Score 9; DB 1; Length 512;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SSPMDTVTE 75
Db 63 SSPMDTVTE 71

RESULT 18
POLY_DROME
ID POLY_DROME STANDARD; PRT; 1035 AA.
AC P10401; P10402;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Retrovirus-related POL polyprotein from transposon gypsy [Contains:
DE Reverse transcriptase (EC 2.7.7.49); Endonuclease].
GN POL.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87064379; PubMed=3023871;
RA Marlor R.L., Parkhurst S.M., Corces V.G.;
RT "The Drosophila melanogaster gypsy transposable element encodes
RT putative gene products homologous to retroviral proteins.";
RL Mol. Cell. Biol. 6:1129-1134(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92293139; PubMed=1318501;
RA Smith P.A., Corces V.G.;
RT "The suppressor of hairy-wing binding region is required for gypsy
RT mutagenesis.";
RL Mol. Gen. Genet. 233:65-70(1992).
RN [3]
RP SEQUENCE OF 21-950 FROM N.A.
RX MEDLINE=86176782; PubMed=2421255;
RA Yuki S., Ishimaru S., Inouye S., Saigo K.;
RT "Identification of genes for reverse transcriptase-like enzymes in

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RT two Drosophila retrotransposons, 412 and gypsy; a rapid detection
RT method of reverse transcriptase genes using YXDD box probes.";
RL Nucleic Acids Res. 14:3017-3030(1986).
CC -----
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CC -----
DR  EMBL; M12927; AAA70219.1; ALT_INIT.
DR  EMBL; X03734; CAA27371.1; -.
DR  PIR; B25666; GNFEGL.
DR  HSSP; P03366; LHMV.
DR  Flybase; FBgn0014966; gypsy/pol.
DR  InterPro; IPR001995; Asp_prot_retrov.
DR  InterPro; IPR000477; RVTse.
DR  InterPro; IPR001584; Rve.
DR  Pfam; PF00665; rve; 1.
DR  Pfam; PF00077; kvp; 1.
DR  Pfam; PF00078; rvt; 1.
KW  Hydrolase; Endonuclease; Transferase; RNA-directed DNA polymerase;
KW  Polyprotein; Transposable element.
FT  CONFLICT 31 32 DA -> AR (IN REF. 3).
FT  CONFLICT 60 60 G -> R (IN REF. 3).
FT  CONFLICT 232 232 F -> S (IN REF. 3).
FT  CONFLICT 490 490 D -> V (IN REF. 3).
FT  CONFLICT 883 883 S -> T (IN REF. 3).
FT  CONFLICT 923 923 N -> S (IN REF. 3).
FT  CONFLICT 947 950 RPIE -> NOLR (IN REF. 3).
SQ  SEQUENCE 1035 AA; 117818 MW; 7B985CA272B8A5A6 CRC64;

Query Match 2.3%; Score 9; DB 1; Length 1035;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 LDLLTQAGV 138
Db 94 LDLLTQAGV 102

RESULT 19
RS17_CHLPN
ID RS17_CHLPN STANDARD; PRT; 86 AA.
AC Q927R6; Q9JQ66;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30S ribosomal protein S17.
GN RPSQ OR RS17 OR CPN0638 OR CP0109.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99208606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Baas S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;

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RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
CC -!- FUNCTION: PROTEIN S17 BINDS SPECIFICALLY TO THE 5' END OF 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE S17P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL; AE001647; AAD18777.1; -;
DR EMBL; AF002173; AAF37992.1; -;
DR EMBL; AF002547; BAA98845.1; -;
DR HSSP; P23828; 1RIP.
DR TIGR; CP0109; -;
DR InterPro; IPR000266; Ribosomal_S17.
DR Pfam; PF00366; Ribosomal_S17; 1.
DR PRINTS; PR00973; RIBOSOMALS17.
DR PRODOM; PD001295; RIBOSOMAL_S17; 1.
DR PROSITE; PS00056; RIBOSOMAL_S17; 1.
KW Ribosomal protein; rRNA-binding; Complete proteome.
SQ SEQUENCE 86 AA; 9889 MW; 7EA25422922FC114 CRC64;

Query Match 2.1%; Score 8; DB 1; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 SEGDKVKI 309
Db 57 SEGDKVKI 64
|||||||

RESULT 20
YC43_PORPU STANDARD; PRT; 254 AA.
AC P51264;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 28.1 kDa protein ycf43 (ORF254).
GN Ycf43.
OS Porphyra purpurea.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Porphyra.
OX NCBI_TaxID=2787;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AVONPORT;
RA Reith M.E., Munholland J.;
RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast genome.";
RL Plant Mol. Biol. Rep. 13:333-335(1995).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE TATC FAMILY.
CC -----
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CC -----
DR EMBL; U38804; AAC08150.1; -;
DR Mendel; I0389; PORPU.ycf43; 1.
DR InterPro; IPR002033; UPF0032.
DR Pfam; PF00902; UPF0032; 1.
DR PROSITE; PS01218; TATC; 1.
KW Chloroplast; Hypothetical protein; Transmembrane.
FT TRANSMEM 41 61 POTENTIAL.
FT TRANSMEM 64 84 POTENTIAL.
FT TRANSMEM 91 111 POTENTIAL.
FT TRANSMEM 125 145 POTENTIAL.
FT TRANSMEM 146 166 POTENTIAL.
FT TRANSMEM 172 192 POTENTIAL.
FT TRANSMEM 204 224 POTENTIAL.
FT TRANSMEM 232 252 POTENTIAL.
SQ SEQUENCE 254 AA; 28149 MW; EE297AE89731AE11 CRC64;

Query Match 2.1%; Score 8; DB 1; Length 254;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 APGEYEFS 273
Db 78 APGEYEFS 85
|||||||

RESULT 21
GOX1_ARATH STANDARD; PRT; 367 AA.
AC Q9LBS0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable (S)-2-hydroxy-acid oxidase, peroxisomal 1 (EC 1.1.3.15) (Glycolate oxidase 1) (GOX 1) (Short chain alpha-hydroxy acid oxidase 1).
DE [1].
GN AT3G14415 OR MLN21.20.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLOMBIA;
RX MEDLINE=20277480; PubMed=10819329;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty P1 and TAC clones.";
RL DNA Res. 7:131-135(2000).
CC -!- CATALYTIC ACTIVITY: (S)-2-hydroxy-acid + O(2) = 2-oxo acid + H(2)O(2).
CC -!- COFACTOR: FMN (BY SIMILARITY).
CC -!- PATHWAY: SECOND REACTION OF THE PHOTORESPIRATORY PATHWAY (GLYCOLATE PATHWAY).
CC -!- SUBUNIT: HOMOTETRAMER OR HOMOOCTAMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Peroxisomal (By similarity).
CC -!- SIMILARITY: BELONGS TO THE FMN-DEPENDENT ALPHA-HYDROXY ACID DEHYDROGENASES FAMILY.
CC -----
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CC -----
DR EMBL; AB028617; BAB01333.1; -.
DR EMBL; AB022220; BAB01333.1; JOINED.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR000262; FMN_hydroxy_acid_dh.
DR Pfam; PF01070; FMN_dh; 1.
DR PROSITE; PS00342; MICROBODIES_C; 1.
DR Oxidoreductase; Flavoprotein; FMN; Peroxisome; Glycolate pathway;
KW Photorespiration.
DR ACT_SITE 24 24 SUBSTRATE BINDING (BY SIMILARITY).
FT ACT_SITE 129 129 SUBSTRATE BINDING (BY SIMILARITY).
FT ACT_SITE 254 254 REMOVES THE SUBSTRATE ALPHA-PROTON AS THE
FT FIRST STEP IN CATALYSIS (BY SIMILARITY).
FT ACT_SITE 257 257 SUBSTRATE BINDING (BY SIMILARITY).
FT SITE 365 367 MICROBODY TARGETING SIGNAL (POTENTIAL).
SQ SEQUENCE 367 AA; 40306 MW; C0H0F9B083F1B6E6 CRC64;

Query Match 2.1%; Score 8; DB 1; Length 367;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 KALALGAS 252
DB 296 KALALGAS 303
|||||

RESULT 22
GOX2_ARATH STANDARD; PRT; 367 AA.
AC Q9LRR9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Probable (S)-2-hydroxy-acid oxidase, peroxisomal 2 (EC 1.1.3.15)
DE (Glycolate oxidase 2) (GOX 2) (Short chain alpha-hydroxy acid oxidase
DE 2).
GN AT3G14420 OR MAO2.2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=2077480; PubMed=10819329;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asanizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones";
RL DNA Res. 7:131-135(2000).
CC -!- CATALYTIC ACTIVITY: (S)-2-hydroxy-acid + O(2) -> 2-oxo acid +
CC H(2)O(2).
CC -!- COFACTOR: FMN (BY SIMILARITY).
CC -!- PATHWAY: SECOND REACTION OF THE PHOTORESPIRATORY PATHWAY
CC (GLYCOLATE PATHWAY).
CC -!- SUBUNIT: HOMOTETRAMER OR HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Peroxisomal (By similarity).
CC -!- SIMILARITY: BELONGS TO THE FMN-DEPENDENT ALPHA-HYDROXY ACID
CC DEHYDROGENASES FAMILY.
CC -----
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CC -----
DR EMBL; AB028617; BAB01334.1; -.

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DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR000262; FMN_hydroxy_acid_dh.
DR Pfam; PF01070; FMN_dh; 1.
DR PROSITE; PS00342; MICROBODIES_CTER; 1.
DR Oxidoreductase; Flavoprotein; FMN; Peroxisome; Glycolate pathway;
KW Photorespiration.
DR ACT_SITE 24 24 SUBSTRATE BINDING (BY SIMILARITY).
FT ACT_SITE 129 129 SUBSTRATE BINDING (BY SIMILARITY).
FT ACT_SITE 254 254 REMOVES THE SUBSTRATE ALPHA-PROTON AS THE
FT FIRST STEP IN CATALYSIS (BY SIMILARITY).
FT ACT_SITE 257 257 SUBSTRATE BINDING (BY SIMILARITY).
FT SITE 365 367 MICROBODY TARGETING SIGNAL (POTENTIAL).
SQ SEQUENCE 367 AA; 40341 MW; B107AD7AC983A04C CRC64;

Query Match 2.1%; Score 8; DB 1; Length 367;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 KALALGAS 252
DB 296 KALALGAS 303
|||||

RESULT 23
Y165_RICPR STANDARD; PRT; 368 AA.
AC Q9ZD28;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein RPl65.
GN RPl65.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sichteritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria";
RL Nature 396:133-140(1998).
CC -----
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CC -----
DR EMBL; AJ235270; CAJ14632.1; -.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 368 AA; 41009 MW; 0410168F891F489C CRC64;

Query Match 2.1%; Score 8; DB 1; Length 368;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 216 AVYKVAEY 223
DB 256 AVYKVAEY 263
|||||

RESULT 24
MDLB_PSEPU

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ID MDLB_PSEPU STANDARD; PRT; 393 AA.
AC P20932;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE L(+)-mandelate dehydrogenase (EC 1.1.1.-) (S-mandelate dehydrogenase)
DE (MDH).
DE MDLB.
GN Pseudomonas putida.
OS Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-30.
RC STRAIN=APCC 12633;
RX MEDLINE=91104894; PubMed=2271624;
RA TSou A.Y., Ransom S.C., Gerlt J.A., Buechter D.D., Babbitt P.C.,
Kenyon G.L.;
RT "Mandelate pathway of Pseudomonas putida: sequence relationships
involving mandelate racemase, (S)-mandelate dehydrogenase, and
benzoylformate decarboxylase and expression of benzoylformate
decarboxylase in Escherichia coli.";
RL Biochemistry 29:9856-9862(1990).
CC -1- FUNCTION: REDUCTION OF L(+)-MANDELATE TO BENZOYLFORMATE.
CC -1- COFACTOR: FMN.
CC -1- PATHWAY: MANDELATE PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE FMN-DEPENDENT ALPHA-HYDROXY ACID
DEHYDROGENASES FAMILY.
-----
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-----
DR EMBL; J05293; AAC15503.1; -.
DR PIR; B44767; B44767.
DR HSSP; P05414; IGOX.
DR InterPro; IPR003109; FMN-enzyme.
DR InterPro; IPR000262; FMN_hydroxy_acid_dh.
DR Pfam; PF01070; FMN_dh; 1.
DR PROSITE; PS00557; FMN_HYDROXY_ACID_DH; 1.
DR Oxidoreductase; Mandelate pathway; Aromatic hydrocarbons catabolism;
KW Flavoprotein; FMN.
FT ACT_SITE 26 26 SUBSTRATE BINDING (BY SIMILARITY).
FT ACT_SITE 131 131 SUBSTRATE BINDING (BY SIMILARITY).
FT ACT_SITE 274 274 REMOVES THE SUBSTRATE ALPHA-PROTON AS THE
FIRST STEP IN CATALYSIS (BY SIMILARITY).
FT ACT_SITE 277 277 SUBSTRATE BINDING (BY SIMILARITY).
SQ SEQUENCE 393 AA; 43437 MW; 18BE23B459BB3987 CRC64;

Query Match 2.1%; Score 8; DB 1; Length 393;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 VKALALGA 251
Db 313 VKALALGA 320
|||||||

RESULT 25
IMDH_HELPJ STANDARD; PRT; 481 AA.
AC Q9ZLL4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
dehydrogenase) (IMPDH) (IMPD).
GN GUAB OR JHP0768.
```

```
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir B.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
-----
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-----
DR EMBL; AE001507; AAD06347.1; -.
DR HSSP; P49058; 1EEP.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN-enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain; Complete proteome.
FT DOMAIN 89 142 CBS 1.
FT DOMAIN 150 204 CBS 2.
FT BINDING 300 300 IMP (POTENTIAL).
SQ SEQUENCE 481 AA; 51688 MW; 688262DCD14EFDAB CRC64;

Query Match 2.1%; Score 8; DB 1; Length 481;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGAS 252
Db 344 KALALGAS 351
|||||||

RESULT 26
IMDH_HELPY STANDARD; PRT; 481 AA.
AC P56088;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
dehydrogenase) (IMPDH) (IMPD).
GN GUAB OR HP0829.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=26695 / ATCC 700392;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Uterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Kar P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RL pylori."
RL Nature 388:539-547(1997).
CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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CC -----
DR EMBL; AE000594; AAC07879.1; -.
DR HSSP; P49058; IEEP.
DR TIGR; HP0829; -.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
DR Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain; Complete proteome.
FT DOMAIN 89 142 CBS 1.
FT DOMAIN 150 204 CBS 2.
FT BINDING 300 300 IMP (POTENTIAL).
SQ SEQUENCE 481 AA; 51802 MW; 075A84B1F8AC9481 CRC64;

Query Match 2.1%; Score 8; DB 1; Length 481;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGAS 252
DB 344 KALALGAS 351
|||||||

RESULT 27
IMDH_AQUAE STANDARD; PRT; 490 AA.
AC O67820;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN GUAB OR AQ.2023.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.B., Overbeek R., Sneed M.A., Keller M., Aujaay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RL Nature 392:353-358(1998).
CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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CC -----
DR EMBL; AE000768; AAC07779.1; -.
DR HSSP; P50099; 1ZPJ.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
DR Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain; Complete proteome.
FT DOMAIN 93 146 CBS 1.
FT DOMAIN 156 210 CBS 2.
FT BINDING 309 309 IMP (POTENTIAL).
SQ SEQUENCE 490 AA; 53400 MW; 66605CDD8B348CE4 CRC64;

Query Match 2.1%; Score 8; DB 1; Length 490;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 PIIADGGI 237
DB 338 PIIADGGI 345
|||||||

RESULT 28
IMDH_RHTR STANDARD; PRT; 498 AA.
AC Q9KH33;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN GUAB.
OS Rhizobium tropici.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=398;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=899;
RA Riccillo P.M., Collavino M.M., Grasso D.H., England R.,
RA de Bruijn F.J., Aguilar M.;
RT "Guab from Rhizobium tropici 899."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
```

```
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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CC -----
CC EMBL: AF272827; AAF85967.1; -.
CC DR HSSP: P49058; IEEP.
CC DR InterPro: IPR000644; CBS.
CC DR InterPro: IPR003009; FMN_enzyme.
CC DR InterPro: IPR001093; IMP_DH_GMP_RED.
CC DR Pfam: PF00571; CBS; 2.
CC DR Pfam: PF00478; IMPDH_C; 1.
CC DR Pfam: PF01574; IMPDH_N; 1.
CC DR SMART: SM00116; CBS; 2.
CC DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
CC KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
CC KW CBS domain.
CC FT DOMAIN 96 150 CBS 1.
CC FT DOMAIN 158 211 CBS 2.
CC FT BINDING 310 310 IMP (POTENTIAL).
CC SQ SEQUENCE 498 AA; 52835 MW; 0A99E38B1078ED73 CRC64;

Query Match 2.1%; Score 8; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 PIIADGGI 237
DB 339 PIIADGGI 346

RESULT 29
ID IMDH_CHLVI
AC G50316; STANDARD; PRT; 521 AA.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN ChloAB.
OS Chlorobium vibrioforme.
OC Bacteria; Green sulfur bacteria; Chlorobium.
OX NCBI_TaxID=1098;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F. THIOSULFATOPHILUM NCIB 8327;
RA Petersen B.L., Moeller M.G., Stummann B.M., Henningsen K.W.;
RT "Clustering of genes with function in the biosynthesis of
RT bacteriochlorophyll and heme in the green sulfur bacterium Chlorobium
RT vibrioforme."
RL Hereditas 125:93-96(1996).
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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CC -----
CC EMBL: Z83933; CAB06303.1; -.
CC DR HSSP: P49058; IEEP.
CC DR InterPro: IPR000644; CBS.
CC DR InterPro: IPR003009; FMN_enzyme.
CC DR InterPro: IPR001093; IMP_DH_GMP_RED.
CC DR Pfam: PF00571; CBS; 2.
CC DR Pfam: PF00478; IMPDH_C; 1.
CC DR Pfam: PF01574; IMPDH_N; 1.
CC DR SMART: SM00116; CBS; 2.
CC DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
CC KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
CC KW CBS domain.
CC FT DOMAIN 118 176 CBS 1.
CC FT DOMAIN 184 237 CBS 2.
CC FT BINDING 336 336 IMP (POTENTIAL).
CC SQ SEQUENCE 521 AA; 56627 MW; 0065FCBC182815A CRC64;

Query Match 2.1%; Score 8; DB 1; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 PIIADGGI 237
DB 365 PIIADGGI 372

RESULT 30
ID Y22B_HAEIN
AC O86223; STANDARD; PRT; 163 AA.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Very hypothetical protein HI0221.1.
GN HI0221.1.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd."
RL Science 269:496-512(1995).
RN [2]
RP IDENTIFICATION.
RA White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D., Peterson J.,
RA Hickey E., Dodson R., Gwinn M.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLE PSEUDOGENE; CORRESPONDS A TANDEM COPY OF THE C-
CC TERMINAL REGION OF GUAB (HI0221).
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
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DR EMBL: U32708; AAC21895.1; -;
 DR HSSP: P50099; 12FJ.
 DR TIGR: HI0221.1; -;
 DR InterPro: IPR001093; IMP_DH_GMP_RED.
 DR Pfam: PF00478; IMPDH_C; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 163 AA; 18406 MW; 04433231582FAC57 CRC64;

Query Match 1.8%; Score 7; DB 1; Length 163;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 YRGMGSL 287
 |||||
 DB 61 YRGMGSL 67

RESULT 31
 IF3_XYLFA STANDARD; PRT; 180 AA.
 AC Q9PFE1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Translation initiation factor IF-3.
 GN INFC OR XF0737.
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Xylella.
 OX NCBI_TaxID=2371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=9A5C;
 RX MEDLINE=20365717; PubMed=10910347;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Quadagno R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
 RT "The genome sequence of the plant pathogen Xylella fastidiosa";
 RL Nature 406:151-159(2000).
 CC -!- FUNCTION: IF-3 BINDS TO THE 30S RIBOSOMAL SUBUNIT AND SHIFTS THE
 CC EQUILIBRIUM BETWEEN 70S RIBOSOMES AND THEIR 50S AND 30S SUBUNITS IN
 CC FAVOR OF THE FREE SUBUNITS, THUS ENHANCING THE AVAILABILITY OF 30S
 CC SUBUNITS ON WHICH PROTEIN SYNTHESIS INITIATION BEGINS.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE IF-3 FAMILY.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE IF-3 FAMILY.
 CC -----

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DR EMBL: AE003916; AAF83547.1; ALT_INIT.
 DR InterPro: IPR001288; IF3.
 DR Pfam: PF00707; IF3; 1.
 DR ProDom: PD002880; IF3; 1.
 DR PROSITE: PS00938; IF3; 1.
 KW Initiation factor; Protein biosynthesis; Complete proteome.
 SQ SEQUENCE 180 AA; 20831 MW; 95F86FB9CE17EF76 CRC64;

Query Match 1.8%; Score 7; DB 1; Length 180;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 EGDVKVI 309
 |||||
 DB 121 EGDVKVI 127

RESULT 32
 IF3_RHOSH STANDARD; PRT; 181 AA.
 ID IF3_RHOSH
 AC O33567;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Translation initiation factor IF-3.
 GN INFC OR PIFC.
 OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
 OC Rhodobacter.
 OX NCBI_TaxID=1063;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
 RX MEDLINE=98036135; PubMed=9370368;
 RA Babic S., Hunter C.N., Rakhlin N.J., Simons R.W., Phillips-Jones M.K.;
 RT "Molecular characterisation of the pifc gene encoding translation
 RT initiation factor 3, which is required for normal photosynthetic
 RT complex formation in Rhodobacter sphaeroides NCIB 8253";
 RL Eur. J. Biochem. 249:564-575(1997).
 CC -!- FUNCTION: IF-3 BINDS TO THE 30S RIBOSOMAL SUBUNIT AND SHIFTS THE
 CC EQUILIBRIUM BETWEEN 70S RIBOSOMES AND THEIR 50S AND 30S SUBUNITS IN
 CC FAVOR OF THE FREE SUBUNITS, THUS ENHANCING THE AVAILABILITY OF 30S
 CC SUBUNITS ON WHICH PROTEIN SYNTHESIS INITIATION BEGINS.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE IF-3 FAMILY.
 CC -----

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DR EMBL: Y14733; CAA75028.1; -;
 DR HSSP: P02999; 2IFE.
 DR InterPro: IPR001288; IF3.
 DR Pfam: PF00707; IF3; 1.
 DR ProDom: PD002880; IF3; 1.
 DR PROSITE: PS00938; IF3; 1.

KW Initiation factor; Protein biosynthesis.
SQ SEQUENCE 181 AA; 20541 MW; 36B720F3BB21BEF4 CRC64;

Query Match 1.8%; Score 7; DB 1; Length 181;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 SEGDKVK 308
|||||||
DB 122 SEGDKVK 128

RESULT 33
PPIA_PSEAE STANDARD; PRT; 187 AA.
ID AC Q59641; Q9HZ13;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Peptidyl-prolyl cis-trans isomerase A precursor (EC 5.2.1.8) (PPIase
A) (Rotamase A) (Cyclophilin A).
GN PPIA OR CYPH OR PA3227.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzer L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen";
RL Nature 406:959-964(2000).
RN [2]

RP SEQUENCE OF 22-175 FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=96146052; PubMed=8581173;
RA Liao X., Charlebois I., Ouellet C., Morency M.J., Dewar K.,
RA Lightfoot J., Foster J., Siehnel R., Schweizer H., Lam J.S.,
RA Hancock R.E., Levesque R.C.;
RT "Physical mapping of 32 genetic markers on the Pseudomonas aeruginosa
RT PA01 chromosome";
RL Microbiology 142:79-86(1996).
CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS. THIS PROTEIN
CC IS NOT ESSENTIAL FOR GROWTH. PRESUMABLY A ROLE IN SIGNAL
CC TRANSDUCTION.
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPETIDES.
CC -1- SUBCELLULAR LOCATION: Periplasmic (Probable).
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -----
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CC -----
DR EMBL; AE004745; AAC06615.1; -;
DR EMBL; X84050; CAA58868.1; -;
DR HSSP; P20752; 1CLH.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMASE.
DR PROSITE; PS00170; CSA_PPIASE_1; FALSE_NEG.

DR PROSITE; PS0072; CSA_PPIASE_2; 1.
KW Isomerase; Rotamase; Periplasmic; Signal; Complete proteome.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 187 PSPTIDYL-PROLYL CIS-TRANS ISOMERASE A.
FT CONFLICT 22 24 TPA -> GTT (IN REF. 2).
FT CONFLICT 173 174 DV -> SL (IN REF. 2).
SQ SEQUENCE 187 AA; 20104 MW; 5664DBC83FB94594 CRC64;

Query Match 1.8%; Score 7; DB 1; Length 187;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 GSLLAAT 263
|||||||
DB 16 GSLLAAT 22

RESULT 34
YBF9_YEAST STANDARD; PRT; 193 AA.
ID YBF9_YEAST
AC P34224;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Hypothetical 22.3 kDa protein in SKT5-SHP1 intergenic region.
GN YBL059W OR YBL0508 OR YBL0516.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=94205266; PubMed=8154187;
RA Scherens B., el Bakkoury M., Vierendeels F., Dubois E., Messenguy F.;
RT "Sequencing and functional analysis of a 32,560 bp segment on the
RT left arm of yeast chromosome II. Identification of 26 open reading
RT frames, including the KIP1 and SEC17 genes";
RL Yeast 9:1355-1371(1993).
RN [2]
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CC -----
DR EMBL; Z23261; CAA80788.1; -;
DR EMBL; Z35820; CAA84879.1; -;
DR PIR; S39829; S39829.
DR PIR; S37330; S37330.
DR SGD; S0000155; YBL059W.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 119 143 POTENTIAL.
SQ SEQUENCE 193 AA; 22278 MW; 891A434C861C1B59 CRC64;

Query Match 1.8%; Score 7; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 GSLLAAT 263
|||||||
DB 121 GSLLAAT 127

RESULT 35
MTR2_MOUSE STANDARD; PRT; 227 AA.
ID MTR2_MOUSE
AC Q92ZD1;
DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Myotubularin-related protein 2 (Fragment).
 GN MTMR2.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98409499; PubMed=9736772;
 RA Laporte J., Blondeau F., Buj-Bello A., Tentler D., Kretz C., Dahl N.,
 RA Mandel J.-L.;
 RT "Characterization of the myotubularin dual specificity phosphatase
 RT gene family from yeast to human.";
 RL Hum. Mol. Genet. 7:1703-1712(1998).
 CC -!- FUNCTION: NOT KNOWN, COULD BE A TYROSINE-PHOSPHATASE.
 CC -!- SIMILARIY: BELONGS TO THE MYOTUBULARIN-LIKE FAMILY.
 CC -----
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 CC -----
 DR EMBL; AF073880; AAC80002.1; -;
 DR MGD; MGI:1924366; Mtnr2.
 DR InterPro; IPR004182; GRAM.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR Pfam; PF02893; GRAM; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; PARTIAL.
 DR PROSITE; PS00056; TYR_PHOSPHATASE_2; PARTIAL.
 KW Hydrolase.
 FT NON_TER 1 1
 FT NON_TER 227 227
 SQ SEQUENCE 227 AA; 25201 MW; 71D540D39AD290C6 CRC64;

 Query Match 1.8%; Score 7; DB 1; Length 227;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 289 AMEKSSS 295
 Db 2 AMEKSSS 8

 RESULT 36
 Y134.METJA
 ID Y134.METJA STANDARD; PRT; 282 AA.
 AC Q57598;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MJ0134.
 GN MJ0134.
 OS Methanococcus jannaschii.
 CC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 CC Methanococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=868087;
 RA Sult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overback R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghagan N.S.M., Weidman J.F., Furmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -!- SIMILARIY: LOW, TO YEAST GCD14.
 CC -----
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 CC -----
 DR EMBL; U67470; AAB98115.1; -;
 DR TIGR; MJ0134; -;
 DR InterPro; IPR001737; RNA_A_dimeth.
 DR InterPro; IPR000051; SAM_bind.
 DR Pfam; PF00398; RnaAad; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 282 AA; 32207 MW; 558FB972B21CFA9C CRC64;

 Query Match 1.8%; Score 7; DB 1; Length 282;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 138 VDVIVILD 144
 Db 182 VDVIVILD 188

 RESULT 37
 YEA5_YEAST
 ID YEA5_YEAST STANDARD; PRT; 282 AA.
 AC P40003;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Hypothetical 31.4 kDa protein in GCNA-WBP1 intergenic region.
 GN YEL005C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
 RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
 RA Chung E., Duncan M., Guzman E., Hartzell G., Hunnicke-Smith S.,
 RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
 RA Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
 RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
 RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC -----
 DR EMBL; U18530; AAB64482.1; -;
 DR SGD; S0000731; VAB2.
 KW Hypothetical protein.
 SQ SEQUENCE 282 AA; 31364 MW; 8F7CA122F91E491A CRC64;

 Query Match 1.8%; Score 7; DB 1; Length 282;
 Best Local Similarity 100.0%; Pred. No. 42;

```
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 SADGLTY 32
    |||||
Db 264 SADGLTY 270

RESULT 38
YC43_GUITH
ID YC43_GUITH STANDARD; PRT; 290 AA.
AC 078493;
DT 15-DEC-1998 (Rel. 37, Created)
DT 13-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 33.1 kDa protein ycf43.
GN YCF43.
OS Guillardia theta (Cryptomonas phi).
OC Chloroplast.
OG
OX NCBI_TaxID=55529;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99128221; PubMed=9929392;
RA Douglas S.E., Penny S.L.;
RT complete sequence and conserved synteny groups confirm its common
    ancestry with red algae.
RL J. Mol. Evol. 48:236-244(1999).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -|- SIMILARITY: BELONGS TO THE TATC FAMILY.
CC
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CC
CC EMBL; AF041468; AAC35684.1;
DR InterPro: IPR002033; UPF0032.
DR Pfam: PF00902; UPF0032; 1.
DR PROSITE: PS01218; TATC; FALSE_NEG.
KW Chloroplast; Hypothetical protein; Transmembrane.
FT TRANSMEM 71 91 POTENTIAL.
FT TRANSMEM 124 144 POTENTIAL.
FT TRANSMEM 155 175 POTENTIAL.
FT TRANSMEM 202 222 POTENTIAL.
FT TRANSMEM 234 254 POTENTIAL.
FT TRANSMEM 262 282 POTENTIAL.
SQ SEQUENCE 290 AA; 33161 MW; CD637821194FAF2F CRC64;

Query Match 1.8%; Score 7; DB 1; Length 290;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 266 APGEYFF 272
    |||||
Db 108 APGEYFF 114

RESULT 39
CD20_HUMAN
ID CD20_HUMAN STANDARD; PRT; 297 AA.
AC P11836; P08984; Q13963;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE B-lymphocyte antigen CD20 (B-lymphocyte surface antigen B1) (Leu-16)
    (Bp35).
DE B-lymphocyte antigen CD20 (B-lymphocyte surface antigen B1) (Leu-16)
    (Bp35).
GN MS4A1 OR CD20.
OS Homo sapiens (Human).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88258386; PubMed=3260267;
RA Stamenkovic I., Seed B.;
RT "Analysis of two cDNA clones encoding the B lymphocyte antigen CD20
    (B1, Bp35), a type III integral membrane protein."
RL J. Exp. Med. 167:1975-1980(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88124792; PubMed=2448768;
RA Tedder T.F., Streuli M., Schlossman S.F., Saito H.;
RT "Isolation and structure of a cDNA encoding the B1 (CD20) cell-surface
    antigen of human B lymphocytes."
RL Proc. Natl. Acad. Sci. U.S.A. 85:208-212(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89176281; PubMed=2466899;
RA Tedder T.F., Klejman G., Schlossman S.F., Saito H.;
RT "Structure of the gene encoding the human B lymphocyte
    differentiation antigen CD20 (B1)."
RL J. Immunol. 142:2560-2568(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=88283639; PubMed=2456210;
RA Einfeld D.A., Brown J.P., Valentine M.A., Clark E.A., Ledbetter J.A.;
RT "Molecular cloning of the human B cell CD20 receptor predicts a
    hydrophobic protein with multiple transmembrane domains."
RL EMBO J. 7:711-717(1988).
CC -|- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN THE REGULATION OF
    B-CELL ACTIVATION AND PROLIFERATION.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- PTM: PHOSPHORYLATED. MIGHT BE FUNCTIONALLY REGULATED BY PROTEIN
    KINASE(S).
CC -|- SIMILARITY: BELONGS TO THE MS4A FAMILY.
CC -|- DATABASE: NAME=PRO; NOTE=CD guide CD20 entry;
    WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd20.htm".
CC
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CC
CC EMBL; X12530; CAA31046.1;
DR EMBL; M27394; AAA35581.1;
DR EMBL; M27395; -; NOT_ANNOTATED_CDS.
DR EMBL; L23419; AAA88911.1;
DR EMBL; L23415; AAA88911.1; JOINED.
DR EMBL; L23416; AAA88911.1; JOINED.
DR EMBL; L23417; AAA88911.1; JOINED.
DR EMBL; X07203; CAA30179.1;
DR EMBL; X07204; CAA30180.1;
DR PIR; A27400; A27400.
DR PIR; J10042; J10042.
DR PIR; A30586; A30586.
DR PIR; S00387; S00387.
DR MIM; 112210;
KW B-cell; Transmembrane; Phosphorylation.
FT DOMAIN 1 63 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 64 84 POTENTIAL.
FT TRANSMEM 85 105 POTENTIAL.
FT TRANSMEM 121 141 POTENTIAL.
FT TRANSMEM 189 209 POTENTIAL.
FT DOMAIN 210 297 CYTOPLASMIC (POTENTIAL).
FT DISULFID 81 167 PROBABLE.
FT DISULFID 167 183 PROBABLE.
FT DISULFID 111 220 PROBABLE.
FT CONFLICT 13 13 P -> L (IN REF. 4).
```


FT CONFLICT 71 M -> I (IN REF. 3).
SQ SEQUENCE 297 AA: 33077 MW: AC5420F8B626BDD1 CRC64;

Query Match 1.8%; Score 7; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 GSLLAAT 263

DB 98 GSLLAAT 104

RESULT 40

PYRD_METJA STANDARD; PRT; 306 AA.
AC Q58070;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Dihydroorotate dehydrogenase (EC 1.3.3.1) (Dihydroorotate oxidase)
DE (DHodehase) (DHODase) (DHOD).
GN PYRD OR MJ0654.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii".
RL Science 273:1058-1073(1996).
CC -!- CATALYTIC ACTIVITY: (S)-dihydroorotate + O(2) = orotate +
H(2)O(2).
CC -!- COFACTOR: FMN (BY SIMILARITY).
CC -!- PATHWAY: FOURTH STEP IN PYRIMIDINE BIOSYNTHESIS.
CC -!- SUBUNIT: HETEROTETRAMER OF 2 PYR AND 2 PYRD SUBUNITS (BY
SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE DIHYDROOROTATE DEHYDROGENASE FAMILY.
CC SUBFAMILY 1.
CC -----
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CC -----
DR EMBL; U67513; AAB98649.1; -;
DR HSP; P54321; 2DOR.
DR TIGR; MJ0654; -;
DR InterPro; IPR001295; DHO_dh.
DR InterPro; IPR003009; FMN_enzyme.
DR Pfam; PF01180; DHodehase; 1.
DR PROSITE; PS00911; DHODEHASE_1; 1.
DR PROSITE; PS00912; DHODEHASE_2; 1.
KW Pyrimidine biosynthesis; Oxidoreductase; Flavoprotein; FMN;
KW Complete proteome.
FT NP_BIND 240 248 FMN (POTENTIAL).
SQ SEQUENCE 306 AA: 32940 MW: E3532389BA9FC7C3 CRC64;

Query Match 1.8%; Score 7; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 DAGVDGL 191

DB 185 DAGVDGL 191

Search completed: September 26, 2002, 08:36:28
Job time: 246 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2002, 08:32:01 ; Search time 28.49 seconds
(without alignments)
2331.697 Million cell updates/sec

Title: US-09-853-918-30
Perfect score: 384
Sequence: 1 MADYLISGGTGYVPEDGLTA.....MSAQIEGGVHGLHYEKRLY 384

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : SPTREMBL_19.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	271	70.6	489	4 Q96NU2	Q96nu2 homo sapien
2	31	8.1	445	11 Q9DC16	Q9dc16 mus musculus
3	31	8.1	514	11 Q91Z11	Q91z11 mus musculus
4	21	5.5	521	3 Q9P8J2	Q9p8j2 candida alb
5	19	4.9	82	11 Q89058	Q89058 mus musculus
6	14	3.6	509	2 Q9RHG9	Q9rhg9 bacillus ce
7	14	3.6	509	2 Q9RHG1	Q9rhg1 bacillus ce
8	13	3.4	499	5 Q9GZH3	Q9gzh3 caenorhabdi
9	13	3.4	524	3 Q14344	Q14344 schizosacch
10	11	2.9	392	10 Q944T1	Q944t1 glycine max
11	11	2.9	502	10 Q9ZPA0	Q9zpa0 glycine max
12	10	2.6	165	4 Q96GP9	Q96gp9 homo sapien
13	10	2.6	485	16 Q9KGN8	Q9kgn8 bacillus ha
14	10	2.6	485	16 Q97FM8	Q97fm8 clostridium
15	10	2.6	501	10 Q9AY75	Q9ay75 oryza sativ
16	10	2.6	742	16 Q930X2	Q930x2 rhizobium m

081282	prunus pers	17	9	2.3	116	10	081282
P78758	schizosacch	18	9	2.3	232	3	P78758
Q9zb97	rhodococcus	19	9	2.3	392	2	Q9zb97
Q9ybu2	aeropyrum p	20	9	2.3	444	17	Q9YBU2
Q9x158	thermotoga	21	9	2.3	482	16	Q9X158
Q9hlx8	thermoplasm	22	9	2.3	485	17	Q9HLK8
Q97814	thermoplasm	23	9	2.3	485	17	Q97814
Q54171	streptomyce	24	9	2.3	495	2	Q54171
Q96387	plasmodym	25	9	2.3	510	5	Q96387
Q9uvl0	pneumocysti	26	9	2.3	529	3	Q9UVL0
Q44384	drosophila	27	9	2.3	1463	5	Q44384
Q9nr9r	leishmania	28	9	2.3	63	5	Q9NR9R
Q41903	arabidopsis	29	8	2.1	86	10	Q41903
Q42831	saccharomyc	30	8	2.1	157	3	Q42831
Q94260	oryza sativ	31	8	2.1	177	10	Q94260
Q97m06	clostridium	32	8	2.1	208	16	Q97M06
Q9d8a8	mus musculu	33	8	2.1	219	11	Q9D8A8
Q81692	medicago sa	34	8	2.1	283	10	Q81692
Q43775	lycopersico	35	8	2.1	290	10	Q43775
Q949t3	arabidopsis	36	8	2.1	298	10	Q949t3
Q9c9k7	arabidopsis	37	8	2.1	302	10	Q9C9K7
Q9zkx2	helicobacte	38	8	2.1	325	16	Q9ZKX2
Q05269	bacillus su	39	8	2.1	326	16	Q05269
Q25523	helicobacte	40	8	2.1	327	16	Q25523
Q99zq1	streptococc	41	8	2.1	327	16	Q99ZQ1
Q97dk4	clostridium	42	8	2.1	327	16	Q97DK4
Q97qg5	streptococc	43	8	2.1	328	16	Q97QG5
Q92bx2	listeria in	44	8	2.1	358	16	Q92BX2
Q9hrm3	halobacteri	45	8	2.1	364	17	Q9HRM3
Q39640	cucurbita s	46	8	2.1	367	10	Q39640
Q944k6	arabidopsis	47	8	2.1	367	10	Q944K6
Q49506	arabidopsis	48	8	2.1	368	10	Q49506
P93260	mesembryant	49	8	2.1	370	10	P93260
Q93n79	streptomyce	50	8	2.1	372	2	Q93N79
Q9ubd6	homo sapien	51	8	2.1	479	4	Q9UBD6
Q9zgd9	streptomyce	52	8	2.1	491	2	Q9ZGD9
Q92rt5	rhizobium m	53	8	2.1	500	16	Q92RT5
Q91017	streptomyce	54	8	2.1	501	2	Q91017
Q86844	streptomyce	55	8	2.1	523	2	Q86844
Q972x2	sulfolobus	56	8	2.1	531	17	Q972X2
Q9ru24	deinococcus	57	8	2.1	594	16	Q9RU24
Q9cxf5	mus musculu	58	8	2.1	700	11	Q9CFX5
Q24749	drosophila	59	8	2.1	1009	5	Q24749
Q9nax5	dictyosteli	60	7	1.8	37	5	Q9NAX5
Q9ulr4	caenorhabdi	61	7	1.8	60	5	Q9ULR4
P70443	mus musculu	62	7	1.8	90	11	P70443
Q50688	borrelia bu	63	7	1.8	91	16	Q50688
Q9jrx5	neisseria m	64	7	1.8	96	16	Q9JRX5
Q9k8a8	bacillus ha	65	7	1.8	104	16	Q9K8A8
Q9js46	neisseria m	66	7	1.8	114	16	Q9JS46
Q9cb10	mycobacteri	67	7	1.8	117	16	Q9CB10
Q9f8p8	carboxydoth	68	7	1.8	130	2	Q9F8P8
Q73496	okra yellow	69	7	1.8	134	12	Q73496
Q9iz49	bhendi yell	70	7	1.8	134	12	Q9IZ49
Q99dr3	chilli leaf	71	7	1.8	134	12	Q99DR3
Q9pgj5	xylella fas	72	7	1.8	135	16	Q9PGJ5
Q9c5f0	libellula q	73	7	1.8	138	8	Q9C5F0
Q9zj49	helicobacte	74	7	1.8	140	16	Q9ZJ49
Q94ar4	arabidopsis	75	7	1.8	143	10	Q94AR4
Q68044	rhodobacter	76	7	1.8	149	2	Q68044
Q9xf99	medicago sa	77	7	1.8	153	10	Q9XF99
Q9ff72	arabidopsis	78	7	1.8	154	10	Q9FF72
Q9ru49	deinococcus	79	7	1.8	166	16	Q9RU49
Q97l92	clostridium	80	7	1.8	179	16	Q97L92
Q9kxt6	streptomyce	81	7	1.8	197	2	Q9KXT6
Q9slp2	carica papa	82	7	1.8	211	10	Q9SLP2
Q9s7g0	arabidopsis	83	7	1.8	217	10	Q9S7G0
Q94jx9	arabidopsis	84	7	1.8	217	10	Q94JX9
Q9zki0	helicobacte	85	7	1.8	217	16	Q9ZKI0
Q9rxn1	deinococcus	86	7	1.8	222	16	Q9RXN1
Q47310	escherichia	87	7	1.8	240	2	Q47310
Q9csb1	mus musculu	88	7	1.8	240	11	Q9CSB1
Q9z912	chlamydia p	89	7	1.8	246	16	Q9Z912

90 049579 arabidopsis
91 023285 arabidopsis
92 255 10 023285
93 092q20 oryza sativ
94 09raq0 leptospira
95 09lca5 bacillus ha
96 09fe89 physcomitre
97 093689 podospora a
98 0960h4 drosophila
99 09x4x5 pseudomonas
100 09pcn7 xylella fas
09cy52 mus musculus

ALIGNMENTS

RESULT 1
ID Q96N02 PRELIMINARY; PRT; 489 AA.
AC Q96N02;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE CDNA FLJ30078 FIS CLONE BGH12000533, HIGHLY SIMILAR TO
DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 2 (EC 1.1.1.205).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Muraoka K., Kanehara K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.,
RA "NEDO human cDNA sequencing project."
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK054640; BAB70780.1; -.
SQ SEQUENCE 489 AA; 52597 MW; 47A1273662A8C39B CRC64;

Query Match 70.6%; Score 271; DB 4; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.6e-276;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 114 LLGAAVGTREDDKYLRLTLTQAGVDVIVLDSQGSNVSQYQIANVHYIKQYPHLQVIGN 173
DB 219 LLGAAVGTREDDKYLRLTLTQAGVDVIVLDSQGSNVSQYQIANVHYIKQYPHLQVIGN 278
QY 174 VVTAQAQNLIDAGVGLRVGMCGSGICITQEVYMACRPGTAVYKVAEYARRFGVPIIA 233
DB 279 VVTAQAQNLIDAGVGLRVGMCGSGICITQEVYMACRPGTAVYKVAEYARRFGVPIIA 338
QY 234 DGGTQTGVHVVKALALGASVVMGSLAATTEAPGEYFFSDGVRLKRYRGMGSLDAMEKS 293
DB 339 DGGTQTGVHVVKALALGASVVMGSLAATTEAPGEYFFSDGVRLKRYRGMGSLDAMEKS 398
QY 294 SSSOKRYFSECDKVKTAQGVSGSIQDKGSIQKFPVYLIAGIQHCCDIGARSLSVLRSM 353
DB 399 SSSOKRYFSECDKVKTAQGVSGSIQDKGSIQKFPVYLIAGIQHCCDIGARSLSVLRSM 458
QY 354 YSGELAFKRTMSAQTEGGVHGLHSYEKRLY 384
DB 459 YSGELAFKRTMSAQTEGGVHGLHSYEKRLY 489
RESULT 2
ID Q9DC16 PRELIMINARY; PRT; 445 AA.
AC Q9DC16;

DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INOSINE 5'-PHOSPHATE DEHYDROGENASE 2.
GN IMPDH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Willing L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
DR EMBL: AK002676; BAB22278.1; -.
DR HSSP: P12268; 1B30.
DR MGD: MGI:109367; Impdh2.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 445 AA; 48474 MW; 1B3A4006640CB4C9 CRC64;

Query Match 8.1%; Score 31; DB 11; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 KALALGASVVMGSLAATTEAPGEYFFSDG 275
DB 306 KALALGASVVMGSLAATTEAPGEYFFSDG 336
RESULT 3
ID Q91211 PRELIMINARY; PRT; 514 AA.
AC Q91211;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE INOSINE 5'-PHOSPHATE DEHYDROGENASE 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC010314; AAH10314.1; -.

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SQ SEQUENCE 514 AA; 55815 MW; 17D25A5C5EBCC439 CRC64;

Query Match
Best Local Similarity 100.08; Pred. No. 1.5e-23; Length 514;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGASTVMGMSLLAATTEAPGYYFFSDG 275
      |||||||
Db 375 KALALGASTVMGMSLLAATTEAPGYYFFSDG 405

RESULT 4
ID Q9P8J2 PRELIMINARY; PRT; 521 AA.
AC Q9P8J2;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE PUTATIVE INOSINE 5-MONOPHOSPHATE DEHYDROGENASE.
GN IMH3.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1006;
RX MEDLINE=20569171; PubMed=11119495;
RA Beckerman J., Chibana H., Turner J., Magee P.T.;
RT "Single-copy IMH3 allele is sufficient to confer resistance to
RT mycophenolic acid in Candida albicans and to mediate transformation of
RT clinical Candida species.";
RL Infect. Immun. 69:108-114.(2001).
DR EMBL; AF249293; AAF70813.1; -.
DR HSSP; P12268; 1B30.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
FT VARIANT 47 47 V -> I.
FT VARIANT 102 102 A -> S.
FT VARIANT 400 400 D -> G.
SQ SEQUENCE 521 AA; 56267 MW; 7A1CF4DF6184FE7E CRC64;

Query Match
Best Local Similarity 100.08; Pred. No. 4.9e-13; Length 521;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 GSICITQEVMAACRPGQTAVY 218
      |||||||
Db 330 GSICITQEVMAACRPGQTAVY 350

RESULT 5
ID O89058 PRELIMINARY; PRT; 82 AA.
AC O89058;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 2 (FRAGMENT).
GN IMPDH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RX MEDLINE=99012997; PubMed=9798653;
RA Chu C.C., Paul W.E.;
RT "Expressed genes in interleukin-4 treated B cells identified by cDNA
RT representational difference analysis.";
RL MOL. Immunol. 35:487-502(1998).
DR EMBL; U89404; AAC36511.1; -.
DR HSSP; P12268; 1B30.
DR MGD; MGI:109367; Impdh2.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00478; IMPDH_C; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 8255 MW; 0ABA6BFD4FAB9964 CRC64;

Query Match
Best Local Similarity 100.08; Pred. No. 1.1e-11; Length 82;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 GGNVVTAAQAKNLIDAGVD 189
      |||||||
Db 1 GGNVVTAAQAKNLIDAGVD 19

RESULT 6
ID Q9RHG9 PRELIMINARY; PRT; 509 AA.
AC Q9RHG9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE IMP DEHYDROGENASE.
GN IMPDH.
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TS-4;
RA Kim S., Miyamoto T., Honjoh K., Iio M., Hatanoto S.;
RT "Molecular cloning, overproduction and characterization of the
RT Bacillus cereus IMP dehydrogenase.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035643; BAA88235.1; -.
DR HSSP; P50099; 1ZFJ.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 509 AA; 55393 MW; 9E6ACB3872C4A451 CRC64;

Query Match
Best Local Similarity 100.08; Pred. No. 1.1e-05; Length 509;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 MDTVTEADMAIAMA 83
      |||||||
Db 51 MDTVTEADMAIAMA 64

RESULT 7
ID Q9RHG1 PRELIMINARY; PRT; 509 AA.
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AC Q9RHG1;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE IMPDH.
GN IMPDH.
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 2152;
RA Kim S., Miyamoto T., Honjoh K., Iio M., Hatano S.;
RT "Molecular cloning, Overproduction and Characterization of the
RT Bacillus cereus."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL; AB036795; BAA89464.1; -;
DR HSSP; P50099; IZFU.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 509 AA; 55194 MW; 77D0C58E2ED62D30 CRC64;

Query Match 3.6%; Score 14; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.le-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 MDTVTEADMAIAMA 83
Db 51 MDTVTEADMAIAMA 64
|||||

RESULT 8
Q9GZH3 PRELIMINARY; PRT; 499 AA.
AC Q9GZH3;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE T22D1.3 PROTEIN.
GN T22D1.3
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT Investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Geisel C., Bradshaw H., Hawkins M.;
RT "The sequence of C. elegans cosmid T22D1.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF030052; AAF98635.1; -;
DR HSSP; P12268; 1B30.

DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 499 AA; 54298 MW; E96323563FE5D275 CRC64;

Query Match 3.4%; Score 13; DB 5; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 LLAATTEAPGEYF 271
Db 395 LLAATTEAPGEYF 407
|||||

RESULT 9
O14344 PRELIMINARY; PRT; 524 AA.
AC O14344;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE PROBABLE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
DE (IMP DEHYDROGENASE) (IMPDH) (IMPD).
GN SPBC2F12.14C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Wood V., Rajandream M.A., Barrell B.G., Skelton J., Churcher C.M.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: INOSINE 5'-PHOSPHATE + NAD(+) + H(2)O =
CC XANTHOSINE 5'-PHOSPHATE + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO GMP
CC REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
DR ENBL; Z97211; CAB10161.1; -;
DR HSSP; P12268; 1B30.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
KW Hypothetical protein; Oxidoreductase; NAD; GMP biosynthesis;
KW Purine biosynthesis; Multigene family; Repeat; CBS domain.
FT DOMAIN 119 174 CBS 1.
FT DOMAIN 182 236 CBS 2.
FT BINDING 337 337 IMP (POTENTIAL).
SQ SEQUENCE 524 AA; 57026 MW; E6C822C22E74674F CRC64;

Query Match 3.4%; Score 13; DB 3; Length 524;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 CITQEVNACGRPQ 213
Db 337 CITQEVNACGRPQ 349
|||||

RESULT 10

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Q944T1
ID Q944T1 PRELIMINARY; PRT; 392 AA.
AC
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE-LIKE PROTEIN (FRAGMENT).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ROOT TIP;
RA Enclayev V., Weschke W., Manteuffel R.;
RT "Study of Gene Expression in Soybean under Aluminium Stress
Conditions.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF421559; AAL18815.1; -.
FT NON_TER 1
SQ SEQUENCE 392 AA; 41872 MW; 9FAD1A0DC5A8BC17 CRC64;

Query Match 2.9%; Score 11; DB 10; Length 392;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 GAAVGTREDDK 127
DB 126 GAAVGTREDDK 136

RESULT 11
Q92PA0 PRELIMINARY; PRT; 502 AA.
AC Q92PA0;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DE INOSINE MONOPHOSPHATE DEHYDROGENASE.
GN IMPDH1.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RA Cao Y., Schubert K.R.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010201; CAB38030.1; -.
DR HSP; P12268; 1B30.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 502 AA; 53407 MW; 617AB87613C36AA4 CRC64;

Query Match 2.9%; Score 11; DB 10; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 GAAVGTREDDK 127
DB 237 GAAVGTREDDK 247

RESULT 12
Q96GP9 PRELIMINARY; PRT; 165 AA.
ID Q96GP9

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AC Q96GP9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE UNKNOWN (PROTEIN FOR MGC:16650).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE, AND RHABDOMYOSARCOMA;
RA Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009321; AAH09321.1; -.
SQ SEQUENCE 165 AA; 17677 MW; 4E47B26055121D80 CRC64;

Query Match 2.6%; Score 10; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADYLIISGTT 10
DB 71 MADYLIISGTT 80

RESULT 13
Q9KGN8 PRELIMINARY; PRT; 485 AA.
AC Q9KGN8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE INOSITOL-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205).
GN GUAB OR BH0020.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001507; BAB03739.1; -.
DR HSP; P50099; 12FJ.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 485 AA; 52429 MW; D0B64489E5CF8B60 CRC64;

Query Match 2.6%; Score 10; DB 16; Length 485;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GVPITADGGI 237
DB 333 GVPITADGGI 342

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RESULT 14
Q97FM8 PRELIMINARY; PRT; 485 AA.
AC Q97FM8;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IMP DEHYDROGENASE.
GN CAC2701.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusev R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL: AE007768; AAK80847.1; -
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Complete proteome.
SQ SEQUENCE 485 AA; 52188 MW; 994D1C5347F7A267 CRC64;

Query Match 2.6%; Score 10; DB 16; Length 485;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GVPIADGGI 237
DB 331 GVPIADGGI 340
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RESULT 15
Q9AY75 PRELIMINARY; PRT; 501 AA.
AC Q9AY75;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE INOSINE MONOPHOSPHATE DEHYDROGENASE.
GN OSJNBA0091J19.1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Buell C.N., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
RA Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSJNBA0091J19 genomic sequence."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC084320; AAK09225.1; -
DR HSSP; P12268; 1B30.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.

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DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 501 AA; 52655 MW; DDE295CB714C3802 CRC64;

Query Match 2.6%; Score 10; DB 10; Length 501;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 GVDGLRVGMG 196
DB 306 GVDGLRVGMG 315
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RESULT 16
Q930X2 PRELIMINARY; PRT; 742 AA.
AC Q930X2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE KINASE/ESTERASE.
GN SMA0137.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymA (megaplasmid 1).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432;
RA Barrett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA Barclay-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire
RT Sinorhizobium meliloti pSymA megaplasmid."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
DR EMBL: AE007201; AAK64730.1; -
KW Kinase; Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 742 AA; 81351 MW; B31AD546F5E81904 CRC64;

Query Match 2.6%; Score 10; DB 16; Length 742;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 ATAMALMGGI 88
DB 27 ATAMALMGGI 36
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RESULT 17
O81282 PRELIMINARY; PRT; 116 AA.
AC O81282;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (FRAGMENT).
OS Prunus persica (Peach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=3760;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. FEICHENG;

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DR HSSP; P12268; 1B30.
DR InterPro; IPR001295; DHO_dh.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR PROSITE; PS00912; DHODEHASE_2; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 444 AA; 47215 MW; 4E3C1C942936905A CRC64;

Query Match      2.3%; Score 9; DB 17; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SSPMDTVTE 75
Db 62 SSPMDTVTE 70

RESULT 21
Q9X168 PRELIMINARY; PRT; 482 AA.
AC Q9X168;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE.
GN TW1347.
OS Thermotoga maritima.
OC Bacteria; Thermotogales; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RL genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
DR EMBL; AE001789; AAD36418.1; -.
DR HSSP; P12268; 1B30.
DR TIGR; TW1347; -.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Complete proteome.
SQ SEQUENCE 482 AA; 52014 MW; 4E08237F69D909FA CRC64;

Query Match      2.3%; Score 9; DB 16; Length 482;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 VPIADGGI 237
Db 329 VPIADGGI 337

RESULT 22
Q9HLK8 PRELIMINARY; PRT; 485 AA.
ID Q9HLK8
AC Q9HLK8;

Query Match      2.3%; Score 9; DB 16; Length 482;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 VPIADGGI 237
Db 329 VPIADGGI 337

RESULT 22
Q9HLK8 PRELIMINARY; PRT; 485 AA.
ID Q9HLK8
AC Q9HLK8;

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DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PROBABLE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE.
GN TA0219.
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaaceae;
OC Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frisman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum.";
RL Nature 407:508-513(2000).
DR EMBL; AL45063; CAC11365.1; -.
DR HSSP; P49058; 1EEP.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 485 AA; 52225 MW; 4450C3DC8FA68673 CRC64;

Query Match      2.3%; Score 9; DB 17; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SSPMDTVTE 75
Db 50 SSPMDTVTE 58

RESULT 23
Q978L4 PRELIMINARY; PRT; 485 AA.
ID Q978L4
AC Q978L4;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IMP DEHYDROGENASE.
GN TVG1445839.
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaaceae;
OC Thermoplasma.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GSSI / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=11121031;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
RA Kawashima T., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic
RT sequence of Thermoplasma volcanium.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
DR EMBL; AP000996; BAB60543.1; -.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.

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DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Complete proteome.
SQ SEQUENCE 485 AA; 52726 MW; 7919D260618917AF CRC64;

Query Match 2.3%; Score 9; DB 17; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 SSPMDTVTE 75
|||||
Db 50 SSPMDTVTE 58

RESULT 24
Q54171 PRELIMINARY; PRT; 495 AA.
AC Q54171;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE OXYGENASE.
GN URDE.
OS Streptomyces fradiae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1906;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TUE2717;
RX MEDLINE=96042088; PubMed=7592377;
RA Decker H., Haag S.;
RT "Cloning and characterization of a polyketide synthase from
Streptomyces fradiae TUE2717 encoding the genes for biosynthesis of
the angucycline antibiotic urdamycin A and a gene probably involved in
its oxygenation.";
RL J. Bacteriol. 177:6126-6136(1995).
DR EMBL; X87093; CAA60567.1; -;
DR InterPro; IPR000733; flavo_monooxygenase.
DR InterPro; IPR002938; MoxY_FAD_binding.
DR InterPro; IPR000205; NAD_binding.
DR InterPro; IPR003042; Rng_monooxygenase.
DR Pfam; PF01494; FAD_binding_3; 1.
DR Pfam; PF01360; Monooxygenase; 1.
DR PRINTS; PR00420; RINGMONOXGNASE.
SQ SEQUENCE 495 AA; 53399 MW; 0F7B9A373A27B700 CRC64;

Query Match 2.3%; Score 9; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 AGVDVIVLD 144
|||||
Db 24 AGVDVIVLD 32

RESULT 25
Q96387 PRELIMINARY; PRT; 510 AA.
AC Q96387;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA Prosise G.L., James A.A., Luecke H.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF035679; AAD10256.1; -;
DR HSSP; P12268; 1B30.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 510 AA; 56148 MW; 449413AD3E41A7D0 CRC64;

Query Match 2.3%; Score 9; DB 5; Length 510;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 ISSPMDTVT 74
|||||
Db 53 ISSPMDTVT 61

RESULT 26
Q9UVL0 PRELIMINARY; PRT; 529 AA.
AC Q9UVL0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE.
OS Pneumocystis carinii.
OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OX NCBI_TaxID=4754;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21125226; PubMed=112323253;
RA Ye D., Lee C.H., Queener S.F.;
RT "Differential splicing of Pneumocystis carinii f. sp. carinii inosine
5'-monophosphate dehydrogenase pre-mRNA.";
RL Gene 263:151-158(2001).
DR EMBL; AF196975; AAF13230.1; -;
DR HSSP; P12268; 1B30.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 529 AA; 58066 MW; 030573A8854ADB5A CRC64;

Query Match 2.3%; Score 9; DB 3; Length 529;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 SSPMDTVTE 75
|||||
Db 77 SSPMDTVTE 85

RESULT 27
O44384 PRELIMINARY; PRT; 1463 AA.
ID O44384;
AC O44384;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PRGAG-POL.
GN GYPSY\POL OR GAG-POL.
OS Drosophila melanogaster (Fruit fly).

```
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Petropoulos C.J.;
RL (in) Coffin J.M. (eds.);
RL Retroviruses, pp.757-757, Cold Spring Harbor Laboratory Press,
RL New York (1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Chappey C.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF033821; AAC82604.1; -.
DR FlyBase; FBgn0014966; gypsy\pol.
DR InterPro; IPR0011995; Asp_prot_retrov.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR000477; Rvtrse.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00077; rvp; 1.
DR Pfam; PF00078; rvt; 1.
DR Pfam; PF00078; rvt; 1.
KW RNA-directed DNA polymerase.
FT CHAIN 1 843
FT CHAIN 844 1463
FT CHAIN PR-RT-RH-IN.
SQ SEQUENCE 1463 AA; 166015 MW; 1A63F7909092E2C7 CRC64;

Query Match 2.3%; Score 9; DB 5; Length 1463;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 LDLLTQAGV 138
Db 522 LDLLTQAGV 530
|||||

RESULT 28
Q9N9R9 ID Q9N9R9 PRELIMINARY; PRT; 63 AA.
AC Q9N9R9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PROBABLE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (FRAGMENT).
GN L2185.10.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Bothe G., Pohl T., Ivens A.C., Quail M., Rajandream M.A.,
RA Barrell B.G.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL; AL358712; CAB94117.2; -.
DR HSSP; P12268; 1B30.
DR InterPro; IPR001053; IMP_DH_GMP_RED.
DR Pfam; PF01574; IMPDH_N; 1.
FT NON_TER 63 63
SQ SEQUENCE 63 AA; 7048 MW; 2315405AF9B78404 CRC64;

Query Match 2.1%; Score 8; DB 5; Length 63;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 DGLTYNDF 35
Db 26 DGLTYNDF 33
|||||

RESULT 29
Q41903 ID Q41903 PRELIMINARY; PRT; 86 AA.
AC Q41903;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (S)-2-HYDROXY-ACID OXIDASE (FRAGMENT).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-GREEN SILIQUES OF A THALIANA ECOTYPE COLUMBIA;
RA Raynal M., Grellier F., Laudie M., Meyer Y., Cooke R., Delsen M.;
RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z17593; CAA79007.1; -.
DR HSSP; P05414; lGOX.
DR InterPro; IPR003009; FMN_enzyme.
FT NON_TER 1 1
SQ SEQUENCE 86 AA; 9420 MW; 452D0A8729FCD727 CRC64;

Query Match 2.1%; Score 8; DB 10; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGAS 252
Db 15 KALALGAS 22
|||||

RESULT 30
O42831 ID O42831 PRELIMINARY; PRT; 157 AA.
AC O42831;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE YAR075WP.
GN YAR075W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C/AB972;
RX MEDLINE=81198945; PubMed=7015287;
RA Page G.S., Hall B.D.;
RT "Characterization of the yeast trna Ser genomic organization and DNA
sequence.";
RL Nucleic Acids Res. 9:921-934(1981).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C/AB972;
RX MEDLINE=84207870; PubMed=6327259;
RA Eigel A., Feldmann H.;
RT "Tyl and delta elements occur adjacent to several trna genes in
yeast.";
RL EMBO J. 1:1245-1250(1982).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C/AB972;
```


RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP003453; BAB68066.1; -; -;
 SQ SEQUENCE 177 AA; 19066 MW; 0EFD31AC74D2608A CRC64;

Query Match 2.1%; Score 8; DB 10; Length 177;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 TPLISSPM 70
 Db 168 TPLISSPM 175
 |||||

RESULT 32
 Q97M06

ID . Q97M06 PRELIMINARY; PRT; 208 AA.
 AC Q97M06;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE DEOXYPHOSPHOGLUCONATE ALDOLASE (GENE KAGA).
 GN CAC0394.

OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum."
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL: AS007554; AAK78374.1; -;
 DR InterPro: IPR000887; Aldlase_KDPC_KHG.
 DR Pfam: PF01081; Aldolase; 1.
 KW Complete proteome.
 SQ SEQUENCE 208 AA; 22457 MW; 15BA9819C74B8346 CRC64;

Query Match 2.1%; Score 8; DB 16; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 VVTAQAQ 181
 Db 71 VVTAQAQ 78
 |||||

RESULT 33
 Q9D8A8

ID Q9D8A8 PRELIMINARY; PRT; 219 AA.
 AC Q9D8A8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE 4432405B04RIK PROTEIN.
 GN 4432405B04RIK.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;

RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Donato M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK008223; BAB25541.1; -;
 DR MGI: 1915228; 4432405B04RIK.
 SQ SEQUENCE 219 AA; 24205 MW; 1775ADS20CCE2892 CRC64;

Query Match 2.1%; Score 8; DB 11; Length 219;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 RLDLTQA 136
 Db 55 RLDLTQA 62
 |||||

RESULT 34
 O81692

ID O81692 PRELIMINARY; PRT; 283 AA.
 AC O81692;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE GLYCOLATE OXIDASE (FRAGMENT).
 OS Medicago sativa (Alfalfa).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
 OX NCBI_TaxID=3879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SHOOT APICAL MERISTEM;
 RA Stout J.M., McKersie B.D.;
 RT "Gene expression in alfalfa."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF082874; AAC32392.1; -;
 DR HSSP: P05414; 1AL8.
 DR InterPro: IPR003009; FMN_enzyme.
 DR InterPro: IPR00262; FMN_hydroxy_acid_dh.
 DR Pfam: PF01070; FMN_dh; 1.
 FT NON_TER 1
 SQ SEQUENCE 283 AA; 30550 MW; F701D54D3B5F56D9 CRC64;

Query Match 2.1%; Score 8; DB 10; Length 283;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGAS 252
 Db 208 KALALGAS 215
 |||||

RESULT 35

Q43775
 ID AC Q43775 PRELIMINARY; PRT; 290 AA.
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE GLYCULATE OXIDASE (EC 1.1.3.15) (FRAGMENT).
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. BREEDING LINE 'DE RUITER 83G38'; TISSUE=LEAF;
 RA Gilpin B.J., Leung D.W., Lancaster J.E.;
 RT "Nucleotide sequence of a nuclear clone of alliinase (Accession No.
 L48614) from onion (PGR95-125).";
 RL Plant Physiol. 110:336-336(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. BREEDING LINE 'DE RUITER 83G38'; TISSUE=LEAF;
 RA Speirs J.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X92888; CAA63482.1; -;
 DR HSSP; P05414; 1AL8.
 DR InterPro; IPR003009; FMN_enzyme.
 DR Pfam; PF01070; FMN_dh; 1.
 DR PROSITE; PS00557; FMN_HYDROXY_ACID_DH; 1.
 KW OXIDOREDUCTASE.
 FT NON_TER 1
 SQ SEQUENCE 290 AA; 31297 MW; 3DC9E093DBF75AB5 CRC64;

Query Match 2.1%; Score 8; DB 10; Length 290;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 KALALGAS 252
 DB 216 KALALGAS 223
 |||||

RESULT 36
 Q949T3 PRELIMINARY; PRT; 298 AA.
 ID AC Q949T3;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE PUTATIVE GLYCULATE OXIDASE.
 GN AT4G18360
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
 RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
 RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Shinn P.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
 RA Shinzaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene AT4G18360 (GI:7268629).";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY050902; AAK93579.1; -;
 SQ SEQUENCE 298 AA; 32308 MW; C16A3E6E80A5AE15 CRC64;

Q43775
 ID AC Q43775 PRELIMINARY; PRT; 290 AA.
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE GLYCULATE OXIDASE (EC 1.1.3.15) (FRAGMENT).
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. BREEDING LINE 'DE RUITER 83G38'; TISSUE=LEAF;
 RA Gilpin B.J., Leung D.W., Lancaster J.E.;
 RT "Nucleotide sequence of a nuclear clone of alliinase (Accession No.
 L48614) from onion (PGR95-125).";
 RL Plant Physiol. 110:336-336(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. BREEDING LINE 'DE RUITER 83G38'; TISSUE=LEAF;
 RA Speirs J.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X92888; CAA63482.1; -;
 DR HSSP; P05414; 1AL8.
 DR InterPro; IPR003009; FMN_enzyme.
 DR Pfam; PF01070; FMN_dh; 1.
 DR PROSITE; PS00557; FMN_HYDROXY_ACID_DH; 1.
 KW OXIDOREDUCTASE.
 FT NON_TER 1
 SQ SEQUENCE 290 AA; 31297 MW; 3DC9E093DBF75AB5 CRC64;

Query Match 2.1%; Score 8; DB 10; Length 290;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 KALALGAS 252
 DB 216 KALALGAS 223
 |||||

RESULT 36
 Q949T3 PRELIMINARY; PRT; 298 AA.
 ID AC Q949T3;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE PUTATIVE GLYCULATE OXIDASE.
 GN AT4G18360
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
 RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
 RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Shinn P.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
 RA Shinzaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene AT4G18360 (GI:7268629).";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY050902; AAK93579.1; -;
 SQ SEQUENCE 298 AA; 32308 MW; C16A3E6E80A5AE15 CRC64;

Query Match 2.1%; Score 8; DB 10; Length 298;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 KALALGAS 252
 DB 226 KALALGAS 233
 |||||

RESULT 37
 Q9C9K7 PRELIMINARY; PRT; 302 AA.
 ID AC Q9C9K7;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE HYPOTHETICAL 30.6 KDA PROTEIN.
 GN F14G6.10.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Altafi H., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altaraj R., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.-J., Koo H.-L., Kremenetskaya I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
 RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana";
 RL Nature 408:816-820(2000).
 DR EMBL; AC015450; AAG51949.1; -;
 DR InterPro; IPR000637; AT_hook.
 DR Pfam; PF02178; AT_hook; 1.
 DR SMART; SM00384; AT_hook; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 302 AA; 30615 MW; 68C755021E3DD375 CRC64;

Query Match 2.1%; Score 8; DB 10; Length 302;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 168 QVIGNVV 175
 DB 197 QVIGNVV 204
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RESULT 38
 Q9ZKZ2 PRELIMINARY; PRT; 325 AA.
 ID AC Q9ZKZ2;
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE GMP REDUCTASE.
 GN GUAC OR JHP0790.

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OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori."
RL Nature 397:176-180(1999).
RL EMBL: AE001509; AAD06382.1; -.
DR HSSP: P12268; 1B30.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
KW Complete proteome.
SQ SEQUENCE 325 AA; 35845 MW; 86F1FCF53DE69E91 CRC64;

Query Match 2.1%; Score 8; DB 16; Length 325;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 PIIADGGI 237
DB 202 PIIADGGI 209

RESULT 39
O05269
ID O05269 PRELIMINARY; PRT; 326 AA.
AC O05269;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYPOTHETICAL 35.8 KDA PROTEIN.
GN YUMD.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Oudega B., Koningssteyn G., Ramon-De Haan M., Rodrigues L.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Boursier R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Chol S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entzian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidos A., Lardinols S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Neone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

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RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z93939; CAB07955.1; -.
DR EMBL: Z99120; CAB15203.1; -.
DR HSSP: P12268; 1B30.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 326 AA; 35819 MW; 4D5EC6F22951D353 CRC64;

Query Match 2.1%; Score 8; DB 16; Length 326;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 PIIADGGI 237
DB 203 PIIADGGI 210

RESULT 40
O25525
ID O25525 PRELIMINARY; PRT; 327 AA.
AC O25525;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GMP REDUCTASE (GUNC).
GN HP0854.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Wathey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
RL EMBL: AE000596; AAD07901.1; -.
DR HSSP: P12268; 1B30.
DR TIGR: HP0854; -.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.

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DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
KW Hypothetical protein: Complete proteome.
SQ SEQUENCE 327 AA; 36038 MW; E9ED3053C3E103C8 CRC64;

Query Match 2.18; Score 8; DB 16; Length 327;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 230 PIIADGGI 237
Db 204 PIIADGGI 211

Search completed: September 26, 2002, 08:36:09
Job time: 248 sec

